

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: December 9, 2001, 09:00:33 ; Search time 258.85 Seconds  
(without alignments)  
9826.865 Million cell updates/sec

Title: US-09-694-777-14  
Perfect score: 2967  
Sequence: 1 atgacctgctggtgggagcag.....gagacatttgagagccagc 2967

Scoring table: IDENTITY-NUC  
Gap 10.0, Gapext 1.0

Searched: 930621 seqs, 428662619 residues  
Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 08  
Maximum Match 1008  
Listing first 45 summaries

Database :

- 1: /SID88/gcgdata/geneseq/geneseqn/NA1980.DAT.\*
- 2: /SID88/gcgdata/geneseq/geneseqn/NA1981.DAT.\*
- 3: /SID88/gcgdata/geneseq/geneseqn/NA1982.DAT.\*
- 4: /SID88/gcgdata/geneseq/geneseqn/NA1983.DAT.\*
- 5: /SID88/gcgdata/geneseq/geneseqn/NA1984.DAT.\*
- 6: /SID88/gcgdata/geneseq/geneseqn/NA1985.DAT.\*
- 7: /SID88/gcgdata/geneseq/geneseqn/NA1986.DAT.\*
- 8: /SID88/gcgdata/geneseq/geneseqn/NA1987.DAT.\*
- 9: /SID88/gcgdata/geneseq/geneseqn/NA1988.DAT.\*
- 10: /SID88/gcgdata/geneseq/geneseqn/NA1989.DAT.\*
- 11: /SID88/gcgdata/geneseq/geneseqn/NA1990.DAT.\*
- 12: /SID88/gcgdata/geneseq/geneseqn/NA1991.DAT.\*
- 13: /SID88/gcgdata/geneseq/geneseqn/NA1992.DAT.\*
- 14: /SID88/gcgdata/geneseq/geneseqn/NA1993.DAT.\*
- 15: /SID88/gcgdata/geneseq/geneseqn/NA1994.DAT.\*
- 16: /SID88/gcgdata/geneseq/geneseqn/NA1995.DAT.\*
- 17: /SID88/gcgdata/geneseq/geneseqn/NA1996.DAT.\*
- 18: /SID88/gcgdata/geneseq/geneseqn/NA1997.DAT.\*
- 19: /SID88/gcgdata/geneseq/geneseqn/NA1998.DAT.\*
- 20: /SID88/gcgdata/geneseq/geneseqn/NA1999.DAT.\*
- 21: /SID88/gcgdata/geneseq/geneseqn/NA2000.DAT.\*
- 22: /SID88/gcgdata/geneseq/geneseqn/NA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2967	100.0	2967	21	Human potassium ion
2	2967	100.0	3083	21	Human eag related
3	2795	94.2	2886	21	Human potassium ion
4	2795	94.2	3002	21	Human eag related
5	1294.4	43.6	2967	22	DNA encoding alpha
6	1294.4	43.6	3289	22	Human ether a gogo
7	432.2	14.6	1434	21	Human secreted pro
8	339.2	11.4	3479	22	Human HERC1 DNA.
9	339.2	11.4	3480	21	Long QT syndrome a
10	339.2	11.4	3950	21	Long QT syndrome a
11	339.2	11.4	4070	22	Human eag-related

12	285.6	9.6	3355	21	AAZ50452
13	281.8	9.5	3857	20	AAZ11906
14	281.4	9.5	3742	21	AAZ93334
15	281.2	9.5	3249	20	AAZ50119
16	281.2	9.5	3323	20	AAZ84910
17	279.6	9.4	3829	21	AAZ87712
18	278	9.4	3252	21	AAZ14893
19	272.8	9.2	3142	20	AAZ56416
20	269.6	9.1	3715	20	AAZ84919
21	244.6	8.2	5107	21	AAZ50455
22	223.6	7.5	3064	20	AAZ84911
23	218	7.3	3736	20	AAZ84918
24	205.8	6.9	3141	20	AAZ56415
25	189	6.4	423	21	AAZ93336
26	149.8	5.0	2694	21	AAZ50453
27	83	2.8	426	22	AAZ16301
28	80.8	2.7	1132	21	AAZ50454
29	76.8	2.6	487	22	AAZ13390
30	76.8	2.6	487	22	AAZ13474
31	68.8	2.3	229	22	AAZ12619
32	66.8	2.3	229	22	AAZ17912
33	66.8	2.3	1995	22	AAZ09558
34	66.6	2.2	470	22	AAZ14351
35	66.6	2.2	470	22	AAZ15725
36	66.6	2.2	470	22	AAZ10481
37	61.6	2.1	936	22	AAZ58252
38	61.6	2.1	936	22	AAZ58254
39	61.6	2.1	936	22	AAZ58257
40	61.6	2.1	936	22	AAZ58259
41	61.6	2.1	936	22	AAZ58262
42	61.6	2.1	938	22	AAZ58255
43	59.4	2.0	2888	20	AAZ09491
44	57.8	1.9	1820	20	AAZ09488
45	57.8	1.9	3431	22	AAZ98302

## ALIGNMENTS

RESULT 1	
AAZ35717	
ID	AAZ35717 standard; cDNA; 2967 BP.
XX	
AC	AAZ35717;
XX	
DT	31-JAN-2000 (first entry)
XX	
DE	Human potassium ion eag channel protein encoding cDNA #2.
XX	
KW	Human; potassium ion eag channel; K+ ion channel; cancer; gene therapy;
KW	neurodegenerative disease; cell proliferation; diagnosis; tumour;
KW	psoriasis; neuroblastoma; cervix carcinoma; carcinoma;
KW	breast adenocarcinoma; breast carcinoma ductal type;
KW	Alzheimer's disease; Parkinson's disease; multiple sclerosis;
KW	lateral amyotrophic sclerosis; ds.
XX	
OS	Homo sapiens.
XX	
PN	W09954463-A2.
XX	
PD	28-OCT-1999.
XX	
PF	21-APR-1999; 99WO-EP02695.
XX	
PR	21-APR-1998; 98EP-0107268.
XX	
PA	(PLAC) MAX PLANCK GES FORDERUNG WISSENSCHAFTEN.
XX	
PI	Pardo-Fernandez IA, Stuehmer W, Beckh S, Brueggemann A;
PI	Del Camino Fernandez-Miranda D, Sanchez Perez A, Weseloh R;
DR	WPI; 2000-013250/01.
DR	P-PSDB; AAY49945.

XX New gene encoding human ion channel useful for diagnosis of, e.g.  
 PT cancer and neurodegenerative diseases -  
 XX  
 PS Claim 1; Page 88-89; 89pp; English.

CC The present sequence encodes a protein (I) having a function of the human  
 CC K<sup>+</sup> (potassium) ion eaq channel. Analysis of the expression of the  
 CC polynucleotide encoding the protein (I) having a function of the human  
 CC K<sup>+</sup> (potassium) ion eaq channel (II) or quantitative presence of  
 CC (I) in cells of mammals such as human, rat or mouse is useful for  
 CC prognosing cancer, neurodegenerative disease and psoriasis. Cancer  
 CC includes neuroblastoma, cervix carcinoma or mamma carcinoma such as  
 CC breast adenocarcinoma or breast carcinoma ductal type. Neurodegenerative  
 CC disease includes Alzheimer's disease, Parkinson's disease, lateral  
 CC amyotrophic sclerosis or multiple sclerosis. By introducing an inhibitor  
 CC of the expression of (II) or an inhibitor or modifying agent of the  
 CC malfunction of (I) or (II) into a mammal disease caused by undesired  
 CC expression or overexpression of (II) or malfunction of (I) can be  
 CC prevented or treated. Inhibitor of the expression of (II) or (I) is also  
 CC useful for inhibiting cell proliferation. (II) can be used in gene  
 CC therapy for inhibiting cell proliferation or disease such as cancer or  
 CC psoriasis and is also useful for specifically detecting human eaq mRNA  
 CC in tissues, by employing the Northern Blot technology. Diagnostic  
 CC compositions are useful in detecting the onset or progress of diseases  
 CC e.g. cancer related to the undesired expression or overexpression of (II)  
 CC and also for detecting malfunction of (I). They are further useful for  
 CC classification of tumours or the developmental status of tumour.

XX Sequence 2967 BP: 735 A; 725 C; 826 G; 681 T; 0 other;

Query Match 100.0%; Score 2967; DB 21; Length 2967;  
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 2967; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgacacatgctggggcaggagggagctagtcgcccctcaacaacagcttctgagagat 60  
 Db 1 atgacacatgctggggcaggagggagctagtcgcccctcaacaacagcttctgagagat 60  
 QY 61 atgttctggcggtccatgataactaatttctgttgggggaatgctcagatgtgacg 120  
 Db 61 atgttctggcggtccatgataactaatttctgttgggggaatgctcagatgtgacg 120  
 QY 121 cctattgtacacgaatgataatgttctgcaagctgctctacacagggcagaagt 180  
 Db 121 cctattgtacacgaatgataatgttctgcaagctgctctacacagggcagaagt 180  
 QY 181 atgcaaaaaaacagacactgagttatgtatgtagggagcgtactgataaagacacg 240  
 Db 181 atgcaaaaaaacagacactgagttatgtatgtagggagcgtactgataaagacacg 240  
 QY 241 gaaaagtgtggcaaacatttgagaactatgagatgaaatcccttgaattctgtac 300  
 Db 241 gaaaagtgtggcaaacatttgagaactatgagatgaaatcccttgaattctgtac 300  
 QY 301 aagaagaacagagacactgtgtgttcttcttgaaatgttccaattcgaaacgaag 360  
 Db 301 aagaagaacagagacactgtgtgttcttcttgaaatgttccaattcgaaacgaag 360  
 QY 361 gataaagtgtttattcttcttgacatttcagtgacaacagcttccaacgcaatt 420  
 Db 361 gataaagtgtttattcttcttgacatttcagtgacaacagcttccaacgcaatt 420  
 QY 421 gaggaatgataatgtaagagctggggaagtctgctggctgacaagagcactgacaag 480  
 Db 421 gaggaatgataatgtaagagctggggaagtctgctggctgacaagagcactgacaag 480  
 QY 481 agcaggggtgtcctgcagcagctgctccaagctgcaaaaagcgagaaatgtccacag 540  
 Db 481 agcaggggtgtcctgcagcagctgctccaagctgcaaaaagcgagaaatgtccacag 540  
 QY 541 caatcccgctgagaggtctctacagctgggtctcagacatccttcccagtaacagaa 600

Db 541 caatcccgctgagaggtctctacagctgggtctcagacatccttcccagtaacagaa 600  
 QY 601 gaggacacaagacccccctacatcatatattgtgttttaagccagctg 660  
 Db 601 gaggacacaagacccccctacatcatatattgtgttttaagccagctg 660  
 QY 661 gatgatcatcttatcttgaccttctctatagacacatttgccttataatgtctc 720  
 Db 661 gatgatcatcttatcttgaccttctctatagacacatttgccttataatgtctc 720  
 QY 721 ttcaaaacaggcagaataatgtgctgtgctgtgttgaagacatcgttgatgtatc 780  
 Db 721 ttcaaaacaggcagaataatgtgctgtgctgtgttgaagacatcgttgatgtatc 780  
 QY 781 ttgtgtggaatgtgtctcaatttatcacacacttgttgagacacagggaggtg 840  
 Db 781 ttgtgtggaatgtgtctcaatttatcacacacttgttgagacacagggaggtg 840  
 QY 841 attctgacccaacttaccgatgaactaccctgaagacgtgtgttgatgacct 900  
 Db 841 attctgacccaacttaccgatgaactaccctgaagacgtgtgttgatgacct 900  
 QY 901 ctgtcctgtttgcatatgtatgtcaacgcttctgaagacgtgagatgagttagtc 960  
 Db 901 ctgtcctgtttgcatatgtatgtcaacgcttctgaagacgtgagatgagttagtc 960  
 QY 961 ttataggtatccacaggagagattgttctgtcatcaaatccaccacactggaggg 1020  
 Db 961 ttataggtatccacaggagagattgttctgtcatcaaatccaccacactggaggg 1020  
 QY 1021 aagaagagtcagagcatcagcagcctgtcagctcctctaaagtgtccgctgcct 1080  
 Db 1021 aagaagagtcagagcatcagcagcctgtcagctcctctaaagtgtccgctgcct 1080  
 QY 1081 ctgtggcaggtgcccgttaagcttgagccactacatgaaatagagctgtgtctgtc 1140  
 Db 1081 ctgtggcaggtgcccgttaagcttgagccactacatgaaatagagctgtgtctgtc 1140  
 QY 1141 ctgtcgt 1200  
 Db 1141 ctgtcgt 1200  
 QY 1201 gggagcatgagatcttctacagagacacacagacatccgacaacagctgctgtac 1260  
 Db 1201 gggagcatgagatcttctacagagacacacagacatccgacaacagctgctgtac 1260  
 QY 1261 caactagcagatgacatttgacaccccttaccagtttaatggtctgtccaggaagt 1320  
 Db 1261 caactagcagatgacatttgacaccccttaccagtttaatggtctgtccaggaagt 1320  
 QY 1321 gaagtgtgtccagagaatctgtctacatctctctgtgtatattcaatgacacg 1380  
 Db 1321 gaagtgtgtccagagaatctgtctacatctctctgtgtatattcaatgacacg 1380  
 QY 1381 gaaagtgtgtccagagaatctgtctacatctctctgtgtatattcaatgacacg 1440  
 Db 1381 gaaagt 1440  
 QY 1441 gggccatcatgataatgtgtcacttctctatgtccacactctcggaatgtgacgact 1500  
 Db 1441 gggccatcatgataatgtgtcacttctctatgtccacactctcggaatgtgacgact 1500  
 QY 1501 atttccacaagatgtatgtccaaacacaaatatacattgagatgtgtccaaagtctcg 1560  
 Db 1501 atttccacaagatgtatgtccaaacacaaatatacattgagatgtgtccaaagtctcg 1560  
 QY 1561 gacttccgaagcttaccaggtgtccaaaggaattgagtgagaggaataatgtatatt 1620  
 Db 1561 gacttccgaagcttaccaggtgtccaaaggaattgagtgagaggaataatgtatatt 1620  
 QY 1621 gtgtccactgtgtccatgtccagagcatgtgacagaaaggtccctgagactgtcccc 1680

Db 1621 gtgtccacttggtccatgctccagagcattgacacagagaaggtccctgcagatctgcccc 1680  
 Oy 1681 aaggaatgagagccgacatctgctgctacactgaaacgcaagtggttcaagagaccccg 1740  
 Db 1681 aaggaatgagagccgacatctgctgctacactgaaacgcaagtggttcaagagaccccg 1740  
 Oy 1741 gctctcgggtggtcgaatgagtggtcctccggcactggtcgaatgttcaagagtg 1800  
 Db 1741 gctctcgggtggtcgaatgagtggtcctccggcactggtcgaatgttcaagagtg 1800  
 Oy 1801 cactgtggtcccaaggagccatctacatgcaagagagagcgttgaagcctctgctt 1860  
 Db 1801 cactgtggtcccaaggagccatctacatgcaagagagagcgttgaagcctctgctt 1860  
 Oy 1861 gtggttctggtcctcctgagtgatccaagatgagtggtggtccatctcagaanaa 1920  
 Db 1861 gtggttctggtcctcctgagtgatccaagatgagtggtggtccatctcagaanaa 1920  
 Oy 1921 gggagacgtgttgagagtggttcttggaagagcaaccccttgccagttccttgccat 1980  
 Db 1921 gggagacgtgttgagagtggttcttggaagagcaaccccttgccagttccttgccat 1980  
 Oy 1981 gttgaggtcctgacactgtgacatgcatggtgacagcgaggtggtccctgcagaagt 2040  
 Db 1981 gttgaggtcctgacactgtgacatgcatggtgacagcgaggtggtccctgcagaagt 2040  
 Oy 2041 ctggaattctacacggtcctcctccatctcctcctccggaacctgattctgacgtacac 2100  
 Db 2041 ctggaattctacacggtcctcctccatctcctcctccggaacctgattctgacgtacac 2100  
 Oy 2101 ttgaggaagagagtggtgttctccggaagatcagcgttgaaagtgaagagagagcgc 2160  
 Db 2101 ttgaggaagagagtggtgttctccggaagatcagcgttgaaagtgaagagagagcgc 2160  
 Oy 2161 atgaagaagaagaatgaggtcccccctgattctgccccggagcccccctggtccgcctc 2220  
 Db 2161 atgaagaagaagaatgaggtcccccctgattctgccccggagcccccctggtccgcctc 2220  
 Oy 2221 ttccagagatctccgacagcagaaagagcagagtcgagtcgagagagaggggagcggagc 2280  
 Db 2221 ttccagagatctccgacagcagaaagagcagagtcgagtcgagagagaggggagcggagc 2280  
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 Db 2281 ctggtatgacatgagtgtgaggaagagggcaatgtccttaacagagcatgtcctccgcaacac 2340  
 Oy 2341 agcctcgtgaaagcgaagcgtgtacccgtgtgagagtcctcgtccagcccgatctcttc 2400  
 Db 2341 agcctcgtgaaagcgaagcgtgtacccgtgtgagagtcctcgtccagcccgatctcttc 2400  
 Oy 2401 caggcaagccctccacccctccgggggtccagacagcaagtcacagcgccgggtccgag 2460  
 Db 2401 caggcaagccctccacccctccgggggtccagacagcaagtcacagcgccgggtccgag 2460  
 Oy 2461 tgcctgggcccacagggggcggtgcatgtgctgcaagcgcaaaagctgggcccgcctc 2520  
 Db 2461 tgcctgggcccacagggggcggtgcatgtgctgcaagcgcaaaagctgggcccgcctc 2520  
 Oy 2521 aaagatgcttcgggggaagtgagtgagtcgaaagagtggtccaaagctgagtcgagtgag 2580  
 Db 2521 aaagatgcttcgggggaagtgagtgagtcgaaagagtggtccaaagctgagtcgagtgag 2580  
 Oy 2581 aacactccgagaggaacaaagcgtcagcgagggccacacgtgaagagagacgactcgtgt 2640  
 Db 2581 aacactccgagaggaacaaagcgtcagcgagggccacacgtgaagagagacgactcgtgt 2640  
 Oy 2641 gaagatgcatcacaagagcagactgctgctgcaacaagtggtgagcagagagagagagagc 2700  
 Db 2641 gaagatgcatcacaagagcagactgctgctgcaacaagtggtgagcagagagagagagagc 2700  
 Oy 2701 cagagatcgagtcacatcctctgcaagagtgcaagatcgttctaccccatcctgagcag 2760  
 Db 2701 cagagatcgagtcacatcctctgcaagagtgcaagatcgttctaccccatcctgagcag 2760

Oy 2761 acgtcgcagggccacagtcctctgagagtgagcagcagctgaaagagagacatcaagcccta 2820  
 Db 2761 acgtcgcagggccacagtcctctgagagtgagcagcagctgaaagagagacatcaagcccta 2820  
 Oy 2821 aacgcaaatgacacatctgagaaacagcctctggaatcctcagatataacttcc 2880  
 Db 2821 aacgcaaatgacacatctgagaaacagcctctggaatcctcagatataacttcc 2880  
 Oy 2881 agaagatcctcagtcctcctcagagagtggttgaataatcagagccacagtcaccagaa 2940  
 Db 2881 agaagatcctcagtcctcctcagagagtggttgaataatcagagccacagtcaccagaa 2940  
 Oy 2941 tcagagagagacatcttctgagagcagc 2967  
 Db 2941 tcagagagagacatcttctgagagcagc 2967  
 Db 2941 tcagagagagacatcttctgagagcagc 2967

RESULT 2  
 AA235722  
 ID AA235722 standard; cDNA: 3083 BP.  
 XX  
 AC AA235722;  
 XX  
 DT 31-JAN-2000 (first entry)  
 XX  
 DE Human eag related gene nucleotide sequence #2.  
 XX  
 KW Human: potassium ion eag channel; K+ ion channel; cancer; gene therapy;  
 KW neurodegenerative disease; cell proliferation; diagnosis; tumour;  
 KW psoriasis; neuroblastoma; cervix carcinoma; carcinoma;  
 KW breast adenocarcinoma; breast carcinoma ductal type;  
 KW Alzheimer's disease; Parkinson's disease; multiple sclerosis;  
 KW lateral amyotrophic sclerosis; ds.  
 KW  
 XX Homo sapiens.  
 XX  
 OS WO954463-A2.  
 XX  
 PN 28-OCT-1999.  
 XX  
 PD 21-APR-1999; 99WO-EP02695.  
 XX  
 PF 21-APR-1998; 98EP-0107268.  
 XX  
 PR (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.  
 XX  
 PA Pardo-Fernandez LA, Stuehmer W, Beckh S, Brueggemann A;  
 PI Del Camino Fernandez-Miranda D, Sanchez Perez A, Weseloh R;  
 XX  
 DR WPI: 2000-013250/01.  
 XX  
 PT New gene encoding human ion channel useful for diagnosis of, e.g.  
 PT cancer and neurodegenerative diseases -  
 XX  
 PS Example 1; Page 73-75; 89pp; English.  
 XX  
 CC The present invention describes proteins (I) having a function of the  
 CC human K+ (potassium) ion eag channel. Analysis of the expression of the  
 CC polynucleotide encoding the protein (I) having a function of the human  
 CC K+ (potassium) ion eag channel (II) or quantitative presence of  
 CC (I) in cells of mammals such as human, rat or mouse is useful for  
 CC diagnosing cancer, neurodegenerative disease and psoriasis. Cancer  
 CC includes neuroblastoma, cervix carcinoma or mamma carcinoma such as  
 CC breast adenocarcinoma or breast carcinoma ductal type. Neurodegenerative  
 CC disease includes Alzheimer's disease, Parkinson's disease, lateral  
 CC amyotrophic sclerosis or multiple sclerosis. By introducing an inhibitor  
 CC of the expression of (II) or an inhibitor or modifying agent of the  
 CC malfunction of (I) or (II) into a mammal disease caused by undesired  
 CC expression or overexpression of (II) or malfunction of (I) can be  
 CC prevented or treated. Inhibitor of the expression of (II) or (I) is also  
 CC useful for inhibiting cell proliferation. (II) can be used in gene  
 CC therapy for inhibiting cell proliferation or disease such as cancer or

CC psoriasis and is also useful for specifically detecting human eag mRNA  
CC in tissues, by employing the Northern Blot technology. Diagnostic  
CC compositions are useful in detecting the onset or progress of diseases  
e.g. cancer related to the undesired expression or overexpression of (11)  
CC and also for detecting malfunction of (1). They are further useful for  
CC classification of tumours or the developmental status of tumour. The  
CC sequence represents a human eag related gene (HKG) nucleotide  
XX  
XX

Sequence 3083 BP; 767 A; 765 C; 852 G; 699 T; 0 other;

Query Match 100.0%; Score 2967; DB 21; Length 3083;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2967; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgacatgctgggggagggagggactagtgccctcaaaacagttcttgagat 60  
DB 37 atgacatgctgggggagggagggactagtgccctcaaaacagttcttgagat 96  
QY 61 atgttcgcgctcccaatgatactaatctgttgggggaatgctcagatagtgactg 120  
DB 97 attgttcgcgctcccaatgatactaatctgttgggggaatgctcagatagtgactg 156  
QY 121 cctattgttacaagcaatgatggaatttgcaggctgtctgctacacagggcagaagt 180  
DB 157 cctattgttacaagcaatgatggaatttgcaggctgtctgctacacagggcagaagt 216  
QY 181 atgcaaaaagcagacactgtcagttttatgtatggggagctgactgataaagacgagt 240  
DB 217 atgcaaaaagcagacactgtcagttttatgtatggggagctgactgataaagacgagt 276  
QY 241 gaaaagtgccgcaaacatttgagaaactatgagaaatcttcgtgaattctgtatc 300  
DB 277 gaaaagtgccgcaaacatttgagaaactatgagaaatcttcgtgaattctgtatc 336  
QY 301 aagaagaacagagacactgtgtgttcttctgtgaaaatgtctcacaatctcgaaaacgacag 360  
DB 337 aagaagaacagagacactgtgtgttcttctgtgaaaatgtctcacaatctcgaaaacgacag 396  
QY 361 gataaagtggtttatttcttcttcgacttcagtgacataacagcttccaagaagcgaat 420  
DB 397 gataaagtggtttatttcttcttcgacttcagtgacataacagcttccaagaagcgaat 456  
QY 421 gagatgatacatgtaaaagctgggggagattgtctcgctgacagagacactgtgacag 480  
DB 457 gagatgatacatgtaaaagctgggggagattgtctcgctgacagagacactgtgacag 516  
QY 481 agcagggtgtctctgacagcagctgtgtccaaagctgtcaaaaagcgagaaatgtccacaag 540  
DB 517 agcagggtgtctctgacagcagctgtgtccaaagctgtcaaaaagcgagaaatgtccacaag 576  
QY 541 cacttcgcctggcgagagtgctcctaagctgggtcagagacatctccccaagtacaagcaa 600  
DB 577 cacttcgcctggcgagagtgctcctaagctgggtcagagacatctccccaagtacaagcaa 636  
QY 601 gaggcacaaagaactcccccctacatactctacatatttggttttaaagccagctg 660  
DB 637 gaggcacaaagaactcccccctacatactctacatatttggttttaaagccagctg 696  
QY 661 gatlgatcatcttgatcttgacactctatacagacatcttgctccctataatgtctcc 720  
DB 697 gatlgatcatcttgatcttgacactctatacagacatcttgctccctataatgtctcc 756  
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DB 877 attctgcacccaactatactcgatgaaactcaggaagctgtgttgtgtgacact 936  
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DB 997 ttatagtgatgccaggagaaatgtgttgtgtgatacgaattccaccacttgagagg 1056  
QY 1021 aagaagatgcaggagcagcagcagctgttccagctctctctctctctctctctctc 1080  
DB 1057 aagaagatgcaggagcagcagcagctgttccagctctctctctctctctctctctc 1116  
QY 1081 ctgggcagatggcccgtaagcttgagacacatactgaatgatggaactgtgtgctgc 1140  
DB 1117 ctgggcagatggcccgtaagcttgagacacatactgaatgatggaactgtgtgctgc 1176  
QY 1141 ctgctgtgtgtgtgttgggtgtgtgacacatgtgactgtgactgtgatacagcat 1200  
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DB 1237 ggggactatgagactcttgacagagacacccaagacaaatccgcaacaacagctgtgtac 1296  
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DB 1297 caactagcgaatgacacttgacaccccttaacagtttaagtggtctgtgctcaggaagt 1356  
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DB 1717 aaggacatgagccgacactgt 1776  
QY 1741 gcttccgctgtgccaagt 1800  
DB 1777 gcttccgctgtgccaagt 1836  
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DB 1897 gtgtgttctgt 1956  
QY 1921 gtagacgtgttggaagatgtgtcttggaaggaagcacccttgccagctctgtgccaat 1980



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Qy 1981 gttgagccttgacctatgtgacatgtatgatcaagcggagatgccttcgaaagt 2040
Dh 2017 gtttaggccttgacctactgtatgtatgtatgtatcaagcggagatgccttcgaaagt 2076
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Dh 2257 ttccagagatctccgacagcagaagaagcagagctgtgcagctggaagaggggcggagac 2316
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Qy 2341 agctctgtgaagcgcagagctgtgacacgtgtgctgagagctcctgcacagccgtatccttc 2400
Dh 2377 agctctgtgaagcgcagagctgtgacacgtgtgctgagagctcctgcacagccgtatccttc 2436
Qy 2401 cagcgaagcctccacctccggggtgcacagacacgaagctacagagcgccagaggtccagag 2460
Dh 2437 cagcgaagcctccacctccggggtgcacagacacgaagctacagagcgccagaggtccagag 2496
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Dh 2557 aaagatccttcgsgaagaagtgagagacgtgaacaagctgtccaaagctgtgagtcgagtgag 2616
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Dh 2797 acgcttgacagcgcacagctcgtgaggtgagcgacagagctgaagagagacatcaagggccta 2856
Qy 2821 aacgcacaaatgacacaatatgtgagaagaacgctccttgagatactcaagatatattcc 2880
Dh 2857 aacgcacaaatgacacaatatgtgagaagaacgctccttgagatactcaagatatattcc 2916
Qy 2881 agaagatccttcagcttccctcagagagtggttgaatatcagagccacagtcctccagaa 2940
Dh 2917 agaagatccttcagcttccctcagagagtggttgaatatcagagccacagtcctccagaa 2976
Qy 2941 tcagagagagacatttttgagacagc 2967
Dh 2977 tcagagagagacatttttgagacagc 3003
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RESULT 3  
AAZ35716

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ID AAZ35716 standard; cDNA; 2886 BP.
XX
AC AAZ35716;
XX
DT 31-JAN-2000 (first entry)
XX
DE Human potassium ion eag channel protein encoding cDNA #1.
XX
KW Human; potassium ion eag channel; K+ ion channel; cancer; gene therapy;
KW neurodegenerative disease; cell proliferation; diagnosis; tumour;
KW psoriasis; neuroblastoma; cervix carcinoma; carcinoma;
KW breast adenocarcinoma; breast carcinoma ductal type;
KW Alzheimer's disease; Parkinson's disease; multiple sclerosis;
KW lateral amyotrophic sclerosis; ds.
XX
OS Homo sapiens.
XX
PN MO954463-A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-EP02695.
XX
PR 21-APR-1998; 98EP-0107268.
XX
PA (PLAC ) MAX PLANCK GRS FOERDERUNG WISSENSCHAFTEN.
PI Pardo-Fernandez LA, Stuehmer W, Beckh S, Brueggemann A;
PI Del Camino Fernandez-Miranda D, Sanchez Perez A, Weseloh R;
XX
DR WPI: 2000-013250/01.
DR P-PSDB: AAY49944.
XX
PT New gene encoding human ion channel useful for diagnosis of, e.g.
XX cancer and neurodegenerative diseases -
XX
PS Claim 1; Page 85-87; 89pp; English.
XX
XX
XX The present sequence encodes a protein (I) having a function of the human
XX K+ (potassium) ion eag channel. Analysis of the expression of the
XX polynucleotide encoding the protein (I) having a function of the human
XX K+ (potassium) ion eag channel (II) or quantitative presence of
XX (I) in cells of mammals such as human, rat or mouse is useful for
XX prognosis cancer, neurodegenerative disease and psoriasis. Cancer
XX includes neuroblastoma, cervix carcinoma or mamma carcinoma such as
XX breast adenocarcinoma or breast carcinoma ductal type. Neurodegenerative
XX disease includes Alzheimer's disease, Parkinson's disease, lateral
XX amyotrophic sclerosis or multiple sclerosis. By introducing an inhibitor
XX of the expression of (II) or an inhibitor or modifying agent of the
XX malfunction of (I) or (II) into a mammal disease caused by undesired
XX expression or overexpression of (II) or malfunction of (I) can be
XX prevented or treated. Inhibitor of the expression of (II) or (I) is also
XX useful for inhibiting cell proliferation. (II) can be used in gene
XX therapy for inhibiting cell proliferation or disease such as cancer or
XX psoriasis and is also useful for specifically detecting human eag mRNA
XX in tissues, by employing the Northern Blot technology. Diagnostic
XX compositions are useful in detecting the onset or progress of diseases
XX e.g. cancer related to the undesired expression or overexpression of (II)
XX and also for detecting malfunction of (I). They are further useful for
XX classification of tumours or the developmental status of tumour.
XX
SQ Sequence 2886 BP; 716 A; 711 C; 799 G; 660 T; 0 other;
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Query Match 94.2%; Score 2795; DB 21; Length 2886;  
Best Local Similarity 97.3%; Pred. No. 0;  
Matches 2886; Conservative 0; Mismatches 0; Indels 81; Gaps 1;

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Dh 1 atgacatggttgaggcgagagagagagtagtggcccttaaaacagttcttgagaat 60
Qy 61 atgttcggcgcgccaatgatactattgtgttgaggagatgctcagatagtgactgg 120
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Db 61 attgttcgctgcccccaatgatactaatcttctgttgggaatgctcagatagtgagctgg 120  
Oy 121 cctatttgtaagaagaatgatgatatttgcgaagctgtctcggctatcacaggaggaagtg 180  
Db 121 cctatttgtaagaagaatgatgatatttgcgaagctgtctcggctatcacaggaggaagtg 180  
Oy 181 atgcataaaagaagcagcacctgcagctttaaatagtgagagctgactatataaagcagact 240  
Db 181 atgcataaaagaagcagcacctgcagctttaaatagtgagagctgactatataaagcagact 240  
Oy 241 gaaaaagtcgagcaaaacatttgaagaactatgagatgaattcctctgnaattctgatatg 300  
Db 241 gaaaaagtcgagcaaaacatttgaagaactatgagatgaattcctctgnaattctgatatg 300  
Oy 301 aagaagaacagagacacccctgtgtgtgtcttctgtgaaaaattgctccaatttgcgaacga 360  
Db 301 aagaagaacagagacacccctgtgtgtgtcttctgtgaaaaattgctccaatttgcgaacga 360  
Oy 361 gataaagtcgtttaaatttctcttcgcaacttcagtgacatacagaacttccaacagccaatt 420  
Db 361 gataaagtcgtttaaatttctcttcgcaacttcagtgacatacagaacttccaacagccaatt 420  
Oy 421 gaggatgatcatatgaagaagctgagggaagttgtctcggctgacaagaagcacttgacaag 480  
Db 421 gaggatgatcatatgaagaagctgagggaagttgtctcggctgacaagaagcacttgacaag 480  
Oy 481 agcagaagtgctctctgcaagaagctgtgctccaagctgacaaagcgagaaatgtcccaag 540  
Db 481 agcagaagtgctctctgcaagaagctgtgctccaagctgacaaagcgagaaatgtcccaag 540  
Oy 541 cactcccgctgagcagaagttccatacagctgagctcagacacccctcccgactacaagca 600  
Db 541 cactcccgctgagcagaagttccatacagctgagctcagacacccctcccgactacaagca 600  
Oy 601 gaggacacaaagactcccccatacatcatcatatgtgttttaagacacagctgg 660  
Db 601 gaggacacaaagactcccccatacatcatcatatgtgttttaagacacagctgg 660  
Oy 661 gatttgatcatcttgaatcttgacactctctatacagccacttggctccctataatgtctcc 720  
Db 661 gatttgatcatcttgaatcttgaatcttgaatcttgaatcttgaatcttgaatcttgaatct 720  
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Db 721 ttcaaaaacagagcagaataatgtgagctgagctgtgtgatagcactgaggaatgtatc 780  
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Oy 961 ttatatgtgataccaggaagatgtgttctgtatcagatttccacacacactgagggg 1020  
Db 961 ttatatgtgataccaggaagatgtgttctgtatcagatttccacacacactgagggg 1020  
Oy 950 ----- 949  
Db 950 ----- 949  
Oy 1021 agagagagtcagagcgaatcagcagcctgttcaagctctctaaagttgtcggctgtccgt 1080  
Db 950 ----- aggcacatcagcagcctgttcaagctctctaaagttgtcggctgtccgt 999  
Oy 1081 cttggcgagtgctgcccgttaagctgagcacaactaatgaaatgagagctgtgtgtgtgtc 1140  
Db 1000 cttggcgagtgctgcccgttaagctgagcacaactaatgaaatgagagctgtgtgtgtgtc 1059  
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Db 1141 cttggcgagtgctgt 1200

Db 1060 ctgctgt 1119  
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Oy 1261 caactaagcagatgagacatctgagcagcccttaacagtttaattggtgtgtgtgtgtgtgtgt 1320  
Db 1180 caactaagcagatgagacatctgagcagcccttaacagtttaattggtgtgtgtgtgtgtgtgt 1239  
Oy 1321 gaagtggt 1380  
Db 1240 gaagtggt 1299  
Oy 1381 ctcaacagctgt 1440  
Db 1300 ctcaacagctgt 1359  
Oy 1441 gtgagcacaatgagatgt 1500  
Db 1360 gtgagcacaatgagatgt 1419  
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Db 1420 atttccacaagaatgtagtgcacaacacacagatatacagatgagatgagatgagatgagatg 1479  
Oy 1561 gacttccagaagctgt 1620  
Db 1480 gacttccagaagctgt 1539  
Oy 1621 gtgtccactgt 1680  
Db 1540 gtgtccactgt 1599  
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Db 1660 gcttccgctgt 1719  
Oy 1801 caactgt 1860  
Db 1720 caactgt 1779  
Oy 1861 gt 1920  
Db 1780 gt 1839  
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Db 1840 ggaagagtggt 1899  
Oy 1981 gtttgggctgt 2040  
Db 1900 gtttgggctgt 1959  
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Oy 2101 ttgaggaagagatgt 2160  
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Oy 2221 ttccaagaattccgacacagcaagaagagcagagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2280  
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 2581 acacttcccgagagcaacaaggcgtcagcgagcgacacacgtgaagaagacagacgtggt 2640  
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 QY 2821 aacgccaatgacacatattgagaacacagctctctgagatactacagataatcctcc 2880  
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 QY 2941 tcagagagagacatttttgagccagc 2967  
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 Db 2860 tcagagagagacatttttgagccagc 2886

AAZ35721  
 ID AAZ35721 standard; cDNA; 3002 BP.  
 AC AAZ35721;  
 XX  
 DT 31-JAN-2000 (first entry)  
 DE Human eag related gene nucleotide sequence #1.  
 XX  
 XX Human; potassium ion eag channel; K+ ion channel; cancer; gene therapy;  
 KW neurodegenerative disease; cell proliferation; diagnosis; tumour;  
 KW psoriasis; neuroblastoma; cervix carcinoma; carcinoma;  
 KW breast adenocarcinoma; breast carcinoma ductal type;  
 KW Alzheimer's disease; Parkinson's disease; multiple sclerosis;  
 KW lateral amyotrophic sclerosis; ds.  
 XX  
 OS Homo sapiens.  
 PN MO9954463-A2.  
 XX  
 PD 28-OCT-1999.  
 XX

PF 21-APR-1999; 99WO-EP02695.  
 XX  
 PR 21-APR-1998; 98EP-0107268.  
 XX  
 PA (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.  
 XX  
 PI Pardo-Fernandez LA, Stuehmer W, Beckh S, Bruggemann A;  
 Del Camino Fernandez-Miranda D, Sanchez Perez A, Weseloh R;  
 DR WPI; 2000-013250/01.

New gene encoding human ion channel useful for diagnosis of, e.g.  
 cancer and neurodegenerative diseases -

Example 1; Page 71-73; 89pp; English.

The present invention describes proteins (I) having a function of the human K+ (potassium) ion eag channel. Analysis of the expression of the polynucleotide encoding the protein (I) having a function of the human K+ (potassium) ion eag channel (II) or quantitative presence of (I) in cells of mammals such as human, rat or mouse is useful for prognosis cancer, neurodegenerative disease and psoriasis. Cancer includes neuroblastoma, cervix carcinoma or mamma carcinoma such as breast adenocarcinoma or breast carcinoma ductal type. Neurodegenerative disease includes Alzheimer's disease, Parkinson's disease, lateral amyotrophic sclerosis or multiple sclerosis. By introducing an inhibitor of the expression of (II) or an inhibitor or modifying agent of the malfunction of (I) or (II) into a mammal disease caused by undesired expression or overexpression of (II) or malfunction of (I) can be prevented or treated. Inhibitor of the expression of (II) or (I) is also useful for inhibiting cell proliferation. (II) can be used in gene therapy for inhibiting cell proliferation or disease such as cancer or psoriasis and is also useful for specifically detecting human eag mRNA in tissues, by employing the Northern Blot technology. Diagnostic compositions are useful in detecting the onset or progress of diseases e.g. cancer related to the undesired expression or overexpression of (II) and also for detecting malfunction of (I). They are further useful for classification of tumours or the developmental status of tumour. The present sequence represents a human eag related gene (HERG) nucleotide sequence from the present invention.

Sequence 3002 BP; 748 A; 751 C; 825 G; 678 T; 0 other;

Query Match 94.2%; Score 2795; DB 21; Length 3002;  
 Best Local Similarity 97.3%; Pred. No. 0;  
 Matches 2886; Conservative 0; Mismatches 0; Indels 81; Gaps 1;

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 Db 37 atgacacatgctggtgggagagagtagtggccctcaaaaacacgtttctggagat 96  
 QY 61 attgttcggcggtcgaatatactatttgtgttggggaatcctcagataggagctgg 120  
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 Db 97 attgttcggcggtcgaatatactatttgtgttggggaatcctcagataggagctgg 156  
 QY 121 cctattgttacagcaatgatgattttgcaagctgtctgcatcacagggagaaigt 180  
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 Db 157 cctattgttacagcaatgatgattttgcaagctgtctgcatcacagggagaaigt 216  
 QY 181 atgcaaaaaagcagcacttgcagtttatgtatgtyggaggtcagatgataagacagatt 240  
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 Db 217 atgcaaaaaagcagcacttgcagtttatgtatgtyggaggtcagatgataagacagatt 276  
 QY 241 gaaaaagtgctggcaaacatttgagaactatgagatgatattcctttgaattctgagtac 300  
 |||||||  
 Db 277 gaaaaagtgctggcaaacatttgagaactatgagatgatattcctttgaattctgagtac 336  
 QY 301 aagaagaacagcagcacttgtgttcttgttgaaaattgctccaattcttgaagaagacag 360  
 |||||||  
 Db 337 aagaagaacagcagcacttgtgttcttgttgaaaattgctccaattcttgaagaagacag 396  
 QY 361 gataaagtggttatttcttcttgcacttccagtgacataacagcttccaacagccaatt 420

Db	397	gataaagtggtttatcttctcttgcaacttccagtcgaatacaacgctttcaacagccaatt	456
OY	421	gaggatgatcatgttaaaagcttggtgggaaagtcttgctcgtgcgaagaagcatcaaacg	480
Db	457	ggagatgatcatgaataaagcttggtgggaaagtcttgctcgtgcgaagaagcatcaaacg	516
OY	481	agcaagggtgtccctgcagcaagcttggtccaagcgtgcgaaaaagcgagaatgttccacaag	540
Db	517	agcaagggtgtccctgcagcaagcttggtccaagcgtgcgaaaaagcgagaatgttccacaag	576
OY	541	cactccgcgctgcgaagaagttccaaagcttggtccaagcgttcctccccgataaagcaa	600
Db	577	cactccgcgctgcgaagaagttccaaagcttggtccaagcgttcctccccgataaagcaa	636
OY	601	gagggcacaaagatccccctcacatcatcttcaattatgtgtttttaagaccagcttg	660
Db	637	gagggcacaaagatccccctcacatcatcttcaattatgtgtttttaagaccagcttg	696
	661	gattgatcatcttgatctctgaaccttcatatacagccaaccttggtcccttaatagtctcc	720
Db	697	gattgatcatcttgatctctgaaccttcatatacagccaaccttggtcccttaatagtctcc	756
OY	721	ttcaaaaccaagcgagaataatgttgcccttggtctgtgtgtatagacatcgtggaattatc	780
Db	757	ttcaaaaccaagcgagaataatgttgcccttggtctgtgtgtatagacatcgtggaattatc	816
OY	781	tttttggtagacatttgctcaaatcttccacaaccttttttgacaagaggggaagtg	840
Db	817	tttttggtagacatttgctcaaatcttccacaaccttttttgacaagaggggaagtg	876
OY	841	attctcgaccccaacttaccgcgatgaactacgtgaagaacgttggttgatgtaacctt	900
Db	877	attctcgaccccaacttaccgcgatgaactacgtgaagaacgttggttgatgtaacctt	936
OY	901	ctgtccctgttcgcataatgatgtcatcaaacgcttttgagaacgttgagtgtaatgtgcc	960
Db	937	ctgtccctgttcgcataatgatgtcatcaaacgcttttgagaacgttgagtgtaatgtgcc	985
OY	961	tttatggtagatcccaaggaaatgtgttcttgcatcagaattccacaacacgtggaagg	1020
Db	986	-----	985
OY	1021	agagagatgcagggcatccagcaagcctgtttcagctctctaaagttgtccgagctgcgt	1080
Db	986	-----agggcatacagcagcctgtttagctctcttaaaagttgtccgagctgcgt	1035
	1081	cttggtcgagttggtcccgtaagcttggaaccactaattgaataatgtagctgtcgtgtgc	1140
Db	1036	cttggtcgagttggtcccgtaagcttggaaccactaattgaataatgtagctgtcgtgtgc	1095
OY	1141	ctgtggtgtgtgtgtgttttggtgcgtgcgtgcacactcgtgatgtgcctgtcatctgtlaagcatt	1200
Db	1096	ctgtggtgtgtgtgtgtgttttggtgcgtgcgtgcacactcgtgatgtgcctgtgtlaagcatt	1155
OY	1201	gggagcatgagagatcttttcgacggagacccaagaacatccgcgaacaacagctgtgttac	1260
Db	1156	gggagcatgagagatcttttcgacggagacccaagaacatccgcgaacaacagctgtgttac	1215
OY	1261	caactagcgatggacattggtcaccccttaccagtttaatggtgtcgtgcagggaaatgtg	1320
Db	1216	caactagcgatggacattggtcaccccttaccagtttaatggtgtcgtgcagggaaatgtg	1275
OY	1321	gaaggtggtgcccgacaagaattctgtctaaatctccctgtgttatcttccaaatgacagc	1380
Db	1276	gaaggtggtgcccgacaagaattctgtctaaatctccctgtgttatcttccaaatgacagc	1335
OY	1381	ctcaaccagttgtggtcttggtgaacatccgcccatccacagacatttgaagaatctttgca	1440
Db	1336	ctcaaccagttgtggtcttggtgaacatccgcccatccacagacatttgaagaatctttgca	1395
OY	1441	gttgccatcatgatgttggtctcaactctctatgtccacacatcttcgggaatgtgacgact	1500

Dd	1396	gtgcccacatcatgatatgttgctcaacttctctatctgccaacatctctccggaaatgttgaacact	1455
Qy	1501	attctcccaacagatgtatgtcccaacacccaacagataccaatgagatgtcttaacagatgttcgg	1560
Dd	1456	attttcccaacagatgtatgtcccaacacccaacagataccatgagatgtctctcaacagatgttcgg	1515
Qy	1561	gaactctcgaagctctaacaggtgtccaaaagatgtagtgagcgagataatgatatatt	1620
Dd	1516	gaactctcgaagctctaacaggtgtccaaaagatgtagtgagcgagataatgatatatt	1575
Qy	1621	gtgtccactgtgtccatgtccgaagagcatatcaaaaagaagaggtcttcgaatctgcgccc	1680
Dd	1576	gtgtccactgtgtccatgtccgaagagcatatcaaaaagaagaggtcttcgaatctgcgccc	1635
Qy	1681	aagagacatgaagcgccgaacatctcgcgtgacacttgaaacccgaagtglttcaagagacccg	1740
Dd	1636	aagagacatgaagcgccgaacatctcgcgtgacacttgaaacccgaagtglttcaagagacccg	1695
Qy	1741	gaccttcggtctgagccagatgatatgtgctctccgggacatctgccaatgagatctccaagtg	1800
Dd	1696	gaccttcggtctgagccagatgatatgtgctctccgggacatctgccaatgagatctccaagtg	1755
Qy	1801	caactgtgccccaggggacctatctatcaatgtgagagagagacggtttgaaagcctctgcctt	1860
Dd	1756	caactgtgccccaggggacctatctatcaatgtgagagagagacggtttgaaagcctctgcctt	1815
Qy	1861	gtggttttcggtgctccctcgagagtgatctcaagaatgactgaggtgtgtgccaatctatagaanaa	1920
Dd	1816	gtggttttcggtgctccctcgagagtgatctcaagaatgactgaggtgtgtgccaatctatagaanaa	1875
Qy	1921	ggagacgtgtttctgagatgtgtctctcgaagaagagccacctctgcagatctctgtgccaat	1980
Dd	1876	ggagacgtgtttctgagatgtgtctctcgaagaagagccacctctgcagatctctgtgccaat	1935
Qy	1981	gttaagggtcttgacctactgttgaatcttgcatagtatcaagcgggatgtgcccttcgagaanaatg	2040
Dd	1936	gttaagggtcttgacctactgttgaatcttgcatagtatcaagcgggatgtgcccttcgagaanaatg	1995
Qy	2041	ctcggaattctaacagggcctctcccatctctctccggaacctgtatctctgaacgtacac	2100
Dd	1996	ctcggaattctaacagggcctctcccatctctctccggaacctgtatctctgaacgtacac	2055
Qy	2101	ttcgaggaagagagatctgtgtctccggaagatctcagcgatgtgaaacgtgaaagagaaacacgc	2160
Dd	2056	ttcgaggaagagagatctgtgtctccggaagatctcagcgatgtgaaacgtgaaagagaaacacgc	2115
Qy	2161	atgaaacgaagaagaatgtagggcccccttgatctctgcccccggaacacactgtccggtgctc	2220
Dd	2116	atgaaacgaagaagaatgtagggcccccttgatctctgcccccggaacacactgtccggtgctc	2175
Qy	2221	ttccaaagaattccggaacagagaagaagaagcgcaagctctgacagctgaaagaagggcgcgagac	2280
Dd	2176	ttccaaagaattccggaacagagaagaagaagcgcaagctctgacagctgaaagaagggcgcgagac	2235
Qy	2281	cttgaatgaactatgatgtgtagaagaagggcaatgtcctctaacagaacgtacctccgccaacac	2340
Dd	2236	cttgaatgaactatgatgtgtagaagaagggcaatgtcctctaacagaacgtacctccgccaacac	2295
Qy	2341	agctctctgtaagggccaagctgtgtctcaacgtgtgtgaagatctctgccaacgcgtatctcttc	2400
Dd	2296	agctctctgtaagggccaagctgtgtgtctcaacgtgtgtgaagatctctgccaacgcgtatctcttc	2355
Qy	2401	cagggaagcctctcaactcccggggttgcacaacacacgaagaagctctacaagcgccaaggtctcag	2460
Dd	2356	cagggaagcctctcaactcccggggttgcacaacacacgaagaagctctacaagcgccaaggtctcag	2415
Qy	2461	tgaccttgagcccaagggggcgggggcgagatgtgtgccaagcggaaagacgtctgggcccccttc	2520
Dd	2416	tgaccttgagcccaagggggcgggggcgagatgtgtgccaagcggaaagacgtctgggcccccttc	2475
Qy	2521	aaagatgtcttcggtgaaagatgtagagactggaacaaagtgtccaagctgtgaatcgatcgtag	2580
Dd	2476	aaagatgtcttcggtgaaagatgtagagactggaacaaagtgtccaagctgtgaatcgatcgtag	2535

QY	2581	acatttcccgagagggacaaaagcgcttaaggcgagggccacacttgaagaagaacagactctgt	26410
Db	2536	acacttcccgagaggaacaagaacgttcaaggcgagggccacacttgaagaagaacagactctgt	25955
QY	2641	gacagtggtccacccaagaagcgactctgcgcctcggaacaacgttggtgaagccagagttcc	27000
Db	2596	gacagtggtccacccaagaagcgactctgcgcctcggaacaacgttggtgaagccagagttcc	26555
QY	2701	ccagatctcgagttcccatctctgtgcagaggtcaagcatctgttctaccccatccctgagcag	27600
Db	2656	ccagatctcgagttcccatctctgtgcagaggtcaagcatctgttctaccccatccctgagcag	27155
QY	2761	acgcttgagggcccaaatctccgtcgagaggtgagagccagcgctgaagaagagatcaaggccta	28200
Db	2716	acgcttgagggcccaaatctccgtcgagaggtgagagccagcgctgaagaagagatcaaggccta	27755
QY	2821	aacgcccacaattgaccacataattggaagaacagcctctctgagatcactcagatattacttcc	28800
Db	2776	aacgcccacaattgaccacataattggaagaacagcctctctgagatcactcagatattacttcc	28355
QY	2881	agaagaatctctcagttctcctcaggaagttgtttgaataatcgagggccacagttccccaag	29400
Db	2836	agaagaatctctcagttctcctcaggaagttgtttgaataatcgagggccacagttccccaag	28955
QY	2941	tcagagagagacatcttttgagcagcagc	2967
Db	2896	tcagagagagacatcttttgagcagcagc	2922
RESULT 5			
AF25271	AAF25271 standard; DNA; 2967 bp.		
AC	AAF25271;		
XX	30-APR-2001 (first entry)		
DE	DNA encoding alpha-subunit of voltage-gated potassium channel (Eag2).		
XX	Alpha-subunit; voltage-gated potassium channel; Eag2; ion flux;		
KW	central nervous system disorder; migraine; hearing; vision; stroke;		
XX	Alzheimer's disease; memory disorder; seizure; psychotic disorder; ss.		
OS	Homo sapiens.		
XX	Key		
XX	Location/Qualifiers		
XX	CDS		
XX	1..2967		
XX	/tag= a		
XX	/product= "Eag2"		
XX	MO200104133-A1.		
XX	18-JAN-2001.		
XX	12-JUL-2000; 2000MO-US18898.		
XX	13-JUL-1999; 99US-0143467.		
XX	(ICAG-) ICAGEN INC.		
XX	Jegla TJ, Liu Y;		
XX	WPI: 2001-138308/14.		
XX	P-PSDB; AAB31714.		
XX	Novel alpha subunit of potassium channel for identifying modulators of the channel for use in treating disorders involving abnormal ion flux, e.g. central nervous system disorders -		
XX	Claim 6; Page 60; 75pp; English.		
XX	The present sequence encodes an alpha-subunit of a voltage-gated		

CC potassium channel. The polypeptide is distributed Ea2. The polypeptide  
CC is useful for screening activators or inhibitors of voltage-gated  
CC potassium channels that contain an Ea2 subunit. Modulators of  
CC voltage-gated channel activity are useful for treating disorders  
CC involving abnormal ion flux, e.g. central nervous system (CNS)  
CC disorders such as migraines, hearing and vision problems, Alzheimer's  
CC disease, learning and memory disorders, seizures, psychotic disorders  
CC and as neuroprotective agents e.g. to prevent stroke. Ea2 is useful  
CC as a reporter molecule to measure changes in potassium concentration,  
CC membrane potential, current flow, ion flux, transcription signal  
CC transduction, receptor-ligand interactions, second messenger  
CC concentration in vitro, in vivo and ex vivo, and also as indicator of  
CC current flow in a particular direction. Detecting Ea2 nucleic acid  
CC and protein expression is useful for diagnosing disease caused by  
CC abnormal ion flux. Ea2 nucleotide and amino acid sequence information  
CC may also be used to construct models of voltage-gated potassium channels  
CC in a computer system.  
XX  
50 Sequence 2967 BP; 853 A; 663 C; 705 G; 746 T; 0 other;  
51

Query Match	43.6%	Score 1294.4;	DB 22;	Length 2967;
Best Local Similarity	67.9%	Pred. No. 0;		
Matches 1993;	Conservative	0;	Mismatches 811;	Indels 132;
			Gaps	8

OY	7	atgctcggggcgaagaggagctatgctgcgccttaaaacagttctcgggaatatgtt	66
Db	1	atgcgcggggcgaagaggcgtcgtgctgcacccgcaagaacatttttgggaacatctgc	60
OY	67	cggcgcccaatgtatacctaattctgtcttggggatcgtcagatagtgagctggccatt	126
Db	61	aggcgctccagttgaatcaagtttcttactcgtggaatgcgccagatcttggatttgcgtga	120
OY	127	gtgtacagcaatgtatgtatcttttgcagaactgtctgtgcataccagggcagaagtgtacaa	186
Db	121	gtttatagttaatgacggtttttgttaaacctctctgatatcatcagtgagtcgtcatcgag	180
OY	187	aaaagcagcactctgcagtttatgtatgtatggggagctgcataagaaacacagattgaaaaa	246
Db	181	aaaagcagcactctgcagtttatgtatgtatggggagattgtacgaagaagaccattgtagaaa	240
OY	247	gtgcggcgaacatttgagaactatgagatgattcctttgaattcttcgatgtacaaag	306
Db	241	gtcagcgcaactcttgcgaactaactgaacaaactgcgtcttggaaagttcttcgtataaadaa	300
OY	307	aacgagacactgtgtgttctctgtgtaaaatctcccaacttcgaaacgaacagatataa	366
Db	301	aacgagacacctgtgtgttctctgttataatgtcaaatctgcaccataagaagaatgacaatgaag	360
OY	367	gtgtgttattattctcttgcacttccagtgcataaacaagcttcaacaagccaatltgagat	426
Db	361	gtgtgtctgtctctgtgtaacttccaagatatlaagttgttttcaacaagccaatagagat	420
OY	427	gattcatgtaaaagctctgggggaagttctgcctgcgtgcacaaagacatcgcacaagcagag	486
Db	421	gattcaacaanaaagcttggagcgaaaatttgcgcgatttgcacagggcttgcacaataagccga	480
OY	487	gggtccgcagcagcgtcggctcacaagcgtgtgaaaaagcgagaaatgcacaagaagcctcc	546
Db	481	aggltttttgcagcagcttcaacgccaa---tgataataacgaaggtgtgtccataacattca	537
OY	547	cgcctggcagaggtgcctacaagctgtgcgtcacaacatactctcccgatgacaagcagaagca	606
Db	538	agactagctgaagttcttctcagctgtgatacagataccttctccagtttaacaagaagc	597
OY	607	ccaaagactccccctacatcatatltacattatgtgttttlaagaccacgttggatttgg	666
Db	598	ccaaagcgcgcacacacacattatttaattatgttgcttttaaaactacttggatttgg	657
OY	667	atcaatcttgatcttgaccttcatacagcaactcttgctccctataatgtctccctcaaa	726
Db	658	gtgattttaatcttctactcttcaacccgaattatgttctctataatgttcttccaa	717









PR 26-MAR-1999: 99US-0126509.  
PR 07-JAN-2000: 2000US-0174853.  
XX  
XX (HOMA-) HUMAN GENOME SCI INC.  
XX  
XX Rosen CA, Ruben SM, Komatsoulis G;  
XX  
XX WPI, 2000-594642/56.  
XX P-PSDB; AAB38242.  
XX  
XX Isolated nucleic acid molecule encoding a human secreted protein is  
XX used in preventing, treating or ameliorating a medical condition -  
XX  
XX Claim 1; Page 354-355; 416pp; English.  
XX  
XX The polynucleotide sequences given in AAC69455 to AAC69502 encode the  
XX human secreted proteins given in AAB38203 to AAB38250. AAB38251 to  
XX AAB38320 represent human secreted polypeptide sequences and proteins  
XX homologous to them, which are given in the exemplification of the present  
XX invention. Human secreted proteins have activities based on the tissues  
XX and cells the genes are expressed in. Example of activities include:  
XX immunosuppressive; antirheumatic; antineoplastic; antiproliferative;  
XX cytostatic; cardiant; vasotropic; cerebroprotective; neurotropic;  
XX neuroprotective; antibacterial; virucide; fungicide; and  
XX ophthalmological. The polynucleotides and polypeptides can be used to  
XX prevent, treat or ameliorate a medical condition in e.g. humans, mice,  
XX rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used  
XX in diagnosing a pathological condition or susceptibility to a  
XX pathological condition. Disorders which are diagnosed or treated include,  
XX autoimmune diseases, hyperproliferative disorders, cardiovascular  
XX disorders, cerebrovascular disorders, angiogenesis, nervous system  
XX disorders, infections caused by bacteria, viruses and fungi and ocular  
XX disorders. The polypeptides can also be used to aid wound healing and  
XX epithelial cell proliferation, to prevent skin aging due to sunburn, to  
XX maintain organs before transplantation, for supporting cell culture of  
XX primary tissues, to regenerate tissues and in chemotaxis. The  
XX polypeptides can also be used as a food additive or preservative to  
XX increase or decrease storage capabilities. AAC69446 to AAC69454 and  
XX AAB38202 represent sequences used in the exemplification of the present  
XX invention.  
XX  
XX Sequence 1434 BP; 423 A; 256 C; 300 G; 452 T; 3 other:  
SQ

Query Match 14.6%; Score 432.2; DB 21; Length 1434;  
Best Local Similarity 99.5%; Pred. No. 4.7e-113;  
Matches 431; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

00 1030 caggcgcacgacgacgtcttcagctctctaaagttgtccggtcctccgtcttgaggcga 1089  
|||  
79 caggcgcacgacgacgtcttcagctctctaaagttgtccggtcctccgtcttgaggcga 138  
00  
QY 1090 gtggccgtacgtctgacccacttaataatgagctgctgctgctgctgctgctgctg 1149  
|||  
Db 139 gtggccgtacgtctgacccacttaataatgagctgctgctgctgctgctgctgctg 198  
|||  
QY 1150 tgtgtgtttggcgtgctgcacacgtgagctgcatctgtgtacagatttgaggact 1209  
|||  
Db 199 tgtgtgtttggcgtgctgcacacgtgagctgcatctgtgtacagatttgaggact 258  
|||

QY 1210 gagatctttgacgaggaacacgaacatccgcaacacagctgtgctgacacactagcg 1269  
|||  
Db 259 gagatctttgacgaggaacacgaacatccgcaacacagctgtgctgacacactagcg 318  
|||

QY 1270 atggaacattgcaaccccttaccagtttaatgggtctgctgacggaagtgggaagtgt 1329  
|||  
Db 319 atggaacattgcaaccccttaccagtttaatgggtctgctgacggaagtgggaagtgt 378  
|||

QY 1330 ccagcgaagaattctgttataatccctcgtgtgtatttccacatacagcctccacagt 1389  
|||  
Db 379 ccagcgaagaattctgttataatccctcgtgtgtatttccacatacagcctccacagt 438  
|||

QY 1390 gtgggctttggaacatcgcccatccacagaacatgtggaagaatcttgcagtggcaltc 1449  
|||

Db 439 gtgggctttggaacatcgcccatccacagaacatgtggaagaatcttgcagtggcaltc 498  
|||  
QY 1450 atgatgatgtgct 1462  
|||  
Db 499 atgatgatgtgct 511  
|||

RESULT 8  
AAH21451  
ID AAH21451 standard; DNA: 3479 BP.  
XX  
XX AAH21451;  
XX  
XX 18-SEP-2001 (first entry)  
XX  
XX Human HERG1 DNA.  
XX  
XX Inhibitor; eukaryotic; potassium channel; TRK1; TRK2; TOK1;  
XX activator; ds.  
XX Homo sapiens.  
XX  
XX MO200151519-A2.  
XX  
XX 19-JUL-2001.  
XX  
XX 05-JAN-2001; 2001MO-EP00055.  
XX  
XX 11-JAN-2000; 2000DE-1000651.  
PR  
XX (AVENTIS PHARMA DEUT GMBH.  
XX Leberer E, Leeuw T, Ritscher A;  
XX  
XX WPI, 2001-442137/47.  
XX  
XX  
XX Identifying inhibitors and activators of eukaryotic potassium channels,  
XX for use as pharmaceuticals, comprises using yeast cells that express  
XX heterologous, but no endogenous, potassium channels -  
XX  
XX  
XX Disclosure; Page 44-45; 78pp; German.  
XX  
XX  
XX This sequence represents a novel method for identifying inhibitors or  
XX activators (A) of a eukaryotic potassium channel (KC) by applying a test  
XX compound to a mutant *Saccharomyces cerevisiae* cell in which: (i) the  
XX three endogenous KC (TRK1, TRK2 and TOK1) are not expressed; but (ii) a  
XX eukaryotic KC is expressed heterologously, where the effect of the  
XX compound on the eukaryotic KC is then determined. The method is used to  
XX identify inhibitors or activators (A) of a eukaryotic potassium channel.  
XX (A) are potentially useful as pharmaceuticals. The method is easily  
XX automated for parallel processing of many samples, using either different  
XX concentrations of test compounds and/or different levels of heterologous  
XX gene expression. It allows identification of compounds that inhibit human  
XX KC selectively. This sequence represents the human HERG1 encoding DNA  
XX described in the method of the invention.  
XX  
XX Sequence 3479 BP; 604 A; 1237 C; 1055 G; 583 T; 0 other:  
SQ

Query Match 11.4%; Score 339.2; DB 22; Length 3479;  
Best Local Similarity 59.0%; Pred. No. 3.2e-86;  
Matches 637; Conservative 0; Mismatches 413; Indels 30; Gaps 2;

QY 1045 cgtttagctctctaaagttgtccggtcctccgtcttgaggcagtgccggaagctg 1104  
|||  
Db 1558 cgttagcgtgctgtaagactgcgcgtctgctggtgtgcgctgcggaagctg 1617  
|||

QY 1105 gaccataacttaataatgagctgctgctgctgctgctgctgctgctgctgctg 1164  
|||  
Db 1618 gactgctacacgaagtaacggtgcgcgtgctgctgctgctgctgctgctgctg 1677  
|||

QY 1165 gtgcacacgtgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 1224  
|||

Db	1678	atcgcgacatgctgtagctgcatactctgtaagcgcatacgaatagagcagccacacatg	1737
Qy	1225	gacacccaagaacatccgcacaacacagctctgtaaccaatacgaatggaatggaacc	1284
Db	1738	gactc-----acgcatactgctctgtaacacaaactggcgacagataagcaaa	1785
Qy	1285	ccctaacgattaatgctgtgtgctcgaaggagtggaagtggtgccagcaagaattct	1344
Db	1786	ccctacaacaacagcagcgctggc-----ggccctccatacaagac	1827
Qy	1345	gtctacatctccctgtgtgtaattccacaatgacagcctcaccagtggtgctttggac	1404
Db	1828	aagatgtgacggcgctcctacttccacttcacagcagcctcacaagtggtgcttgcgaac	1887
Qy	1405	atcgccccaatccacaagacatttgaagaatccttgcagaatgagccatacatgatgtgtca	1464
Db	1888	gtctctcccaacccaactcagaagaatctcttcacatgctgcatatgctatgtgtcc	1947
Qy	1465	cttctctatgcccacatcttcgggaatgtgagacatcttctccaacagatgatgtccac	1524
Db	1948	ctcatgtatgcttagcaatcttcggcaacgtgtgcggccatccataccaacggtgtaaccgggc	2007
Qy	1525	accacaacgataccaatgatagatagtgccacaacagtggttcgggaacttcctgaagctcacaagtg	1588
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RESULT 9			
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ID AAA07601 standard; DNA: 3480 BP.			
XX AAA07601;			
XX 20-JUN-2000 (first entry)			
DT Long QT syndrome associated HERG gene coding region.			
DE			

KW	HERG; mutation; long QT syndrome; LQT syndrome; gene therapy; human; ds.
XX	
OS	Homo sapiens.
FH	
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FT	
FT	mutation
FT	1955
FT	/tag= e
FT	/note= "the nucleotide at this position can be altered to C; specifically claimed for in claim 1"
PX	
PN	WO200006772-A1.
PD	
PP	10-FEB-2000.
XP	
PP	20-JUL-1999; 99WO-US16337.
XX	
XX	27-JUL-1998; 98US-0122847.
PR	06-JAN-1999; 99US-0226012.
XX	
PA	(UTAH ) UNIV UTAH RES FOUND.
XI	
PI	Keating MT, Splawski I;
DR	WPI: 2000-195319/17.
DR	P-PSDB; AAY85405.
XX	
PT	New isolated mutant HERG nucleic acids, useful for developing products for the diagnosis, prevention and treatment of long QT syndrome -
PS	
XX	Claim 1; Fig 8A-B; 16pp: English.
CC	
CC	The invention relates to a HERG protein having a mutation compared to wild-type HERG, and is useful for developing products for the diagnosis, prevention and treatment of long QT (LQT) syndrome. The products and methods can be used for the diagnosis of subjects with LQT syndrome. They can also be used to screen for drugs for treating or preventing LQT syndrome. The HERG nucleic acids can also be used for gene therapy and HERG peptides can be used for peptide therapy. The present sequence represents the coding region of the LQT syndrome associated HERG gene. The HERG gene sequence comprising any of the following mutations apart from those indicated above is specifically claimed for in the specification. The mutations can be selected from C87A, A98C, C132A, G140T, G157C, G167A, T196G, A209G, C215A, G232C, DEU221-251, duplicate C234-250, C241T, T257G, insert C422-423, insert C453-454, insert C724-725, delG888, C934T, C1039T, G1128A, A1129-2G, G1592A, T1655C, G1681A, G1750A, G1755T, T1778C, G1810A, G1825A, C1838T, C1843G, G1876A, C1881G, C1894T, A1912G, del 1913-1915, A1933T, G2044T, insert T2218-2219, C2254T, del C2395, G2398+4C, G2338+1C, T2414C, T2414G, C3467T, A2582T, G2592+1A, del G2660, C2750T, del G2762, C2764T, insert G2775-2776, del G2906, del 2959-2960, G3003A, C3040T, del C3094 and insert C3303-3304.
XX	
SQ	Sequence 3480 BP: 604 A: 1237 C: 1056 G: 583 T: 0 other:

Query Match      11.4%    Score 339.2    DB 21: Length 3480.

Best Local Similarity 59.0%; Pred. No. 3.2e-86;  
Matches 637; Conservative 0; Mismatches 413; Indels 30; Gaps 2;

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QY 1525 accaacaataacacacacacacacacacacacacacacacacacacacacacacac 1584
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## RESULT 10

AAA07602  
ID AAA07602 standard; cDNA: 3950 BP.

AC AAA07602;

DT 19-JUN-2000 (first entry)

DE Long QT syndrome associated HERG protein encoding cDNA.

KW HERG; mutation; long QT syndrome; LQT syndrome; gene therapy; human; ss.

XX Homo sapiens.

OS WO200006772-A1.

PD 10-FEB-2000.

PF 20-JUL-1999; 99WO-US16337.

PR 27-JUL-1998; 98US-0122847.

PR 06-JAN-1999; 99US-0226012.

PA (UTAH ) UNIV UTAH RES FOUND.

PI Keating MT, Splawski I;

DR WPI; 2000-195319/17.

DR P-PSDB; AAY85406.

PT New isolated mutant HERG nucleic acids, useful for developing products for the diagnosis, prevention and treatment of long QT syndrome -

PS Disclosure; Fig 8A-B; 163pp; English.

CC The invention relates to a HERG protein having a mutation compared to wild-type HERG, and is useful for developing products for the diagnosis, prevention and treatment of long QT (LQT) syndrome. The products and methods can be used for the diagnosis of subjects with LQT syndrome. They can also be used to screen for drugs for treating or preventing LQT syndrome. The HERG nucleic acids can also be used for gene therapy and CC HERG peptides can be used for peptide therapy. The present sequence represents the LQT syndrome associated HERG protein encoding cDNA.

XX Sequence 3950 BP; 695 A; 1369 C; 1210 G; 676 T; 0 other;

Query Match 11.4%; Score 339.2; DB 21; Length 3950;

Best Local Similarity 59.0%; Pred. No. 3.5e-86;  
Matches 637; Conservative 0; Mismatches 413; Indels 30; Gaps 2;

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Chr	Start (Mb)	End (Mb)	Gene	Transcript	Accession	Length (bp)	GC (%)	GC3 (%)	GC4 (%)	GC5 (%)	GC6 (%)	GC7 (%)	GC8 (%)	GC9 (%)	GC10 (%)	GC11 (%)	GC12 (%)	GC13 (%)	GC14 (%)	GC15 (%)	GC16 (%)	GC17 (%)	GC18 (%)	GC19 (%)	GC20 (%)	GC21 (%)	GC22 (%)	GC23 (%)	GC24 (%)	GC25 (%)	GC26 (%)	GC27 (%)	GC28 (%)	GC29 (%)	GC30 (%)	GC31 (%)	GC32 (%)	GC33 (%)	GC34 (%)	GC35 (%)	GC36 (%)	GC37 (%)	GC38 (%)	GC39 (%)	GC40 (%)	GC41 (%)	GC42 (%)	GC43 (%)	GC44 (%)	GC45 (%)	GC46 (%)	GC47 (%)	GC48 (%)	GC49 (%)	GC50 (%)	GC51 (%)	GC52 (%)	GC53 (%)	GC54 (%)	GC55 (%)	GC56 (%)	GC57 (%)	GC58 (%)	GC59 (%)	GC60 (%)	GC61 (%)	GC62 (%)	GC63 (%)	GC64 (%)	GC65 (%)	GC66 (%)	GC67 (%)	GC68 (%)	GC69 (%)	GC70 (%)	GC71 (%)	GC72 (%)	GC73 (%)	GC74 (%)	GC75 (%)	GC76 (%)	GC77 (%)	GC78 (%)	GC79 (%)	GC80 (%)	GC81 (%)	GC82 (%)	GC83 (%)	GC84 (%)	GC85 (%)	GC86 (%)	GC87 (%)	GC88 (%)	GC89 (%)	GC90 (%)	GC91 (%)	GC92 (%)	GC93 (%)	GC94 (%)	GC95 (%)	GC96 (%)	GC97 (%)	GC98 (%)	GC99 (%)	GC100 (%)	GC101 (%)	GC102 (%)	GC103 (%)	GC104 (%)	GC105 (%)	GC106 (%)	GC107 (%)	GC108 (%)	GC109 (%)	GC110 (%)	GC111 (%)	GC112 (%)	GC113 (%)	GC114 (%)	GC115 (%)	GC116 (%)	GC117 (%)	GC118 (%)	GC119 (%)	GC120 (%)	GC121 (%)	GC122 (%)	GC123 (%)	GC124 (%)	GC125 (%)	GC126 (%)	GC127 (%)	GC128 (%)	GC129 (%)	GC130 (%)	GC131 (%)	GC132 (%)	GC133 (%)	GC134 (%)	GC135 (%)	GC136 (%)	GC137 (%)	GC138 (%)	GC139 (%)	GC140 (%)	GC141 (%)	GC142 (%)	GC143 (%)	GC144 (%)	GC145 (%)	GC146 (%)	GC147 (%)	GC148 (%)	GC149 (%)	GC150 (%)	GC151 (%)	GC152 (%)	GC153 (%)	GC154 (%)	GC155 (%)	GC156 (%)	GC157 (%)	GC158 (%)	GC159 (%)	GC160 (%)	GC161 (%)	GC162 (%)	GC163 (%)	GC164 (%)	GC165 (%)	GC166 (%)	GC167 (%)	GC168 (%)	GC169 (%)	GC170 (%)	GC171 (%)	GC172 (%)	GC173 (%)	GC174 (%)	GC175 (%)	GC176 (%)	GC177 (%)	GC178 (%)	GC179 (%)	GC180 (%)	GC181 (%)	GC182 (%)	GC183 (%)	GC184 (%)	GC185 (%)	GC186 (%)	GC187 (%)	GC188 (%)	GC189 (%)	GC190 (%)	GC191 (%)	GC192 (%)	GC193 (%)	GC194 (%)	GC195 (%)	GC196 (%)	GC197 (%)	GC198 (%)	GC199 (%)	GC200 (%)	GC201 (%)	GC202 (%)	GC203 (%)	GC204 (%)	GC205 (%)	GC206 (%)	GC207 (%)	GC208 (%)	GC209 (%)	GC210 (%)	GC211 (%)	GC212 (%)	GC213 (%)	GC214 (%)	GC215 (%)	GC216 (%)	GC217 (%)	GC218 (%)	GC219 (%)	GC220 (%)	GC221 (%)	GC222 (%)	GC223 (%)	GC224 (%)	GC225 (%)	GC226 (%)	GC227 (%)	GC228 (%)	GC229 (%)	GC230 (%)	GC231 (%)	GC232 (%)	GC233 (%)	GC234 (%)	GC235 (%)	GC236 (%)	GC237 (%)	GC238 (%)	GC239 (%)	GC240 (%)	GC241 (%)	GC242 (%)	GC243 (%)	GC244 (%)	GC245 (%)	GC246 (%)	GC247 (%)	GC248 (%)	GC249 (%)	GC250 (%)	GC251 (%)	GC252 (%)	GC253 (%)	GC254 (%)	GC255 (%)	GC256 (%)	GC257 (%)	GC258 (%)	GC259 (%)	GC260 (%)	GC261 (%)	GC262 (%)	GC263 (%)	GC264 (%)	GC265 (%)	GC266 (%)	GC267 (%)	GC268 (%)	GC269 (%)	GC270 (%)	GC271 (%)	GC272 (%)	GC273 (%)	GC274 (%)	GC275 (%)	GC276 (%)	GC277 (%)	GC278 (%)	GC279 (%)	GC280 (%)	GC281 (%)	GC282 (%)	GC283 (%)	GC284 (%)	GC285 (%)	GC286 (%)	GC287 (%)	GC288 (%)	GC289 (%)	GC290 (%)	GC291 (%)	GC292 (%)	GC293 (%)	GC294 (%)	GC295 (%)	GC296 (%)	GC297 (%)	GC298 (%)	GC299 (%)	GC300 (%)	GC301 (%)	GC302 (%)	GC303 (%)	GC304 (%)	GC305 (%)	GC306 (%)	GC307 (%)	GC308 (%)	GC309 (%)	GC310 (%)	GC311 (%)	GC312 (%)	GC313 (%)	GC314 (%)	GC315 (%)	GC316 (%)	GC317 (%)	GC318 (%)	GC319 (%)	GC320 (%)	GC321 (%)	GC322 (%)	GC323 (%)	GC324 (%)	GC325 (%)	GC326 (%)	GC327 (%)	GC328 (%)	GC329 (%)	GC330 (%)	GC331 (%)	GC332 (%)	GC333 (%)	GC334 (%)	GC335 (%)	GC336 (%)	GC337 (%)	GC338 (%)	GC339 (%)	GC340 (%)	GC341 (%)	GC342 (%)	GC343 (%)	GC344 (%)	GC345 (%)	GC346 (%)	GC347 (%)	GC348 (%)	GC349 (%)	GC350 (%)	GC351 (%)	GC352 (%)	GC353 (%)	GC354 (%)	GC355 (%)	GC356 (%)	GC357 (%)	GC358 (%)	GC359 (%)	GC360 (%)	GC361 (%)	GC362 (%)	GC363 (%)	GC364 (%)	GC365 (%)	GC366 (%)	GC367 (%)	GC368 (%)	GC369 (%)	GC370 (%)	GC371 (%)	GC372 (%)	GC373 (%)	GC374 (%)	GC375 (%)	GC376 (%)	GC377 (%)	GC378 (%)	GC379 (%)	GC380 (%)	GC381 (%)	GC382 (%)	GC383 (%)	GC384 (%)	GC385 (%)	GC386 (%)	GC387 (%)	GC388 (%)	GC389 (%)	GC390 (%)	GC391 (%)	GC392 (%)	GC393 (%)	GC394 (%)	GC395 (%)	GC396 (%)	GC397 (%)	GC398 (%)	GC399 (%)	GC400 (%)	GC401 (%)	GC402 (%)	GC403 (%)	GC404 (%)	GC405 (%)	GC406 (%)	GC407 (%)	GC408 (%)	GC409 (%)	GC410 (%)	GC411 (%)	GC412 (%)	GC413 (%)	GC414 (%)	GC415 (%)
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[illegible]



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Qy 1885 atccaaagtatgagtggtgtggtcactcttaggaaagagagcgtgttggagatgtgttc 1944
Db 2551 ctgcggggcgcagctgcgtcgtgcacatctctggggaatgacatcttggggagcctctg 2610
Qy 1945 tggaggaagacacacccctgtccctgctgtgcacatgttgaagcctgacactgactgtat 2004
Db 2611 aacctgtatgcaagcctgtgcgaagtgcgaagggatgtgcggccctccactactgtgac 2670
Qy 2005 ctgcattgtgacagcggagtgccctgcagaaagtgtctgaattctacacggtcctctcc 2064
Db 2671 ctacacaaagtctcatcgtgcagcctgtcgtgaggtgtctgacatgtaccctgagttccc 2730
Qy 2065 catctctctcccggaacctgattctgacgtacaaacttgaaggaagatgtgttccgg 2124
Db 2731 gaccacttctgtgcagcgtcgtgagatcactcactcagactcgagataacacatgatcccg 2790

RESULT 12
AAZ50452 standard; cDNA; 3355 BP.
AC AAZ50452:
XX 18-MAY-2000 (first entry)
DE Monkey potassium channel molecule ERG-LP1 cDNA.
XX
KW Monkey: potassium channel molecule; ERG-like protein 1; ERG-LP1;
KW neuroprotective; antiParkinsonian; anticonvulsant; antidepressant;
KW neuroleptic; nootropic; treatment; CNS disorder; central nervous system;
KW potassium channel mediated disorder; epilepsy; Alzheimer's disease;
KW Parkinson's; multiple sclerosis; depression; schizophrenia; amnesia; ss.
XX
OS Primates.
XX
FH Key Location/Qualifiers
FT 5'UTR 1..103
FT /tag= a
FT CDS 104..3355
FT /tag= D
FT /product= "ERG-LP1"
FT /note= "this region is specifically claimed"
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PN W0200005346-A1.
XX
ED 03-FEB-2000.
XX
PF 21-JUL-1999; 99WO-US16752.
XX
PR 21-JUL-1998; 98US-0119855.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Curtis RAD;
XX
DR WPI: 2000-182682/16.
DR P-PSDB: AAY44904.
XX
PT Novel gene encoding potassium channel molecule useful in treating
PT central nervous system disorders such as Alzheimer's disease, multiple
PT sclerosis, and schizophrenia
XX
PS Claim 2; Fig 1; 144pp; English.
XX
CC The present sequence is a cDNA encoding ERG-like protein 1 (ERG-LP1)
CC which is a member of ERG potassium channel family. This sequence is
CC from a full length clone j1kb25d10 which was derived from monkey
CC hippocampal library. ERG-LP1 is expressed exclusively in the brain.
CC Highest expression is found in cortical regions, hippocampus, caudate
CC and amygdala. The protein functions as a potassium channel modulator and
CC has neuroprotective, antiParkinsonian, anticonvulsant, antidepressant,
CC neuroleptic and nootropic activities. The present sequence is
CC useful for treating several potassium channel mediated disorders (CNS
CC disorders) such as Alzheimer's disease, Parkinson's disease, multiple
CC sclerosis, epilepsy, depression, schizophrenic disorders and amnesia.
XX
SQ Sequence 3355 BP; 580 A; 1128 C; 1041 G; 606 T; 0 other;
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Query Match 9.6%; Score 285.6; DB 21; Length 3355;
Best Local Similarity 49.8%; Pred. No. 6,8e-71;
Matches 1051; Conservative 0; Mismatches 989; Indels 72; Gaps 10;

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Qy 75 caatg-----atactatttgtgttggggaatgctcagatagtg---actggcctat 125
Db 169 cgacggcaagcagcaagtaacttctgtcgtgcaacgcgccagcgtggtgggtctctcccg 228
Qy 126 tgtgtacagcaatgattgatttgcgaagctctctggtctatacgaaggcagaagtgtgca 185
Db 229 gttctactgctgtatgtgtcttgcacactcagcggtcttcccggtcgtgagtgatgca 288
Qy 186 aaaaagcagcactcagtttatgtatggtggagctgactgtataagaacatgtaaaa 245
Db 289 gcggggctgtgctgtctcttcccttatgtggcagacacacagtgagctgttcgcgaaaa 348
Qy 246 agtgcggcaaacatttggagaactatgataatcttcttgaaattctgtatcaaga 305
Db 349 gatccgcaagccctcgagagacacaaagaggttcaagctgtgactgttaccggaa 408
Qy 306 gaacggacacactgtgtgttcttcttgaaaaattgtccaaatctgcaaaagcaagataa 365
Db 409 gagcgggtcccggtctgtgtgtctcgtgatgtgatacccaataaagaatgagaaggga 468
Qy 366 agtgtttatttcttgcacttcaatgtagacataacagcttcaaacagcca----- 417
Db 469 gttgtctcttctctagctctcacaagaacatcagtgaaacaaagacggggggcc 528
Qy 418 -----atgaagatgattcatgtaaagcgtgggggaagttgtctg-----ctgaca 466
Db 529 tgacagatggaagagagaaagtagtgcgcggcgcgatatgtgcgggacgataccaaag 588
Qy 467 gagcactgacaagcagcagggggtgtctcctgcaag-cagctgtgctccaaagctgcaaaaagc 525
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D	b		589	c t t c a a g t g c c a a c c g c g g c g g g a g c c g g g c t g t c t c t a c c a c c g t c c g g a c c t y c a	648
O	y		526	g a g a a t g t l c c a a c a a g a g c t c c c g c t g y g a g a g t l c t c a c a g c t g y g e t c a g a c a c t c t	585
D	b		649	g a a g c a g c c c a a g g g c a a g a c a a g c t c a a t a a g g g g t g t t g g g a g a a c c a a c t t	708
O	y		586	- c c c c a g t a c a a g a a g a a g c a c c a a a g a t c c c c t c a t c a l c a t t a c t a t i a t i g t g t	644
D	b		709	g c c t g a g a t c a a a a g t a g c t g c a c c g a a g t o c g c t t t c a t c c t g t g c a c t y g y g g c	768
O	y		645	t t t a a g a c c a c g y g g g a t t g s a t c a t t t g a t t t g a t a c t t a c a c c a t t g a c c a t t g t	704
D	b		769	g c t g a g g c c a c c c t g y g a t g c t t c a c t g c t c g c a c g c t a t g t y g c t y t a c c g t	828
O	y		705	c c c t a t a a t g t c t c t c t c a a a c c a g a a a t a y f g s c t a t g t c g c t y g t t g t a g	764
D	b		829	g c c t a a c a g c g t g t g t g t g a g c a a c a g g a g a c c c a g t g c c g c c g g c c a c c a g	888
O	y		765	c a t c - - - - - g t g a t g t a t c t t t t g t g t a c a t g t g t c a t t t t c a t a	812
D	b		889	c g t c t g a c c t g c t g t g a a g t c t c t c t t c a t c c t g s a t t g c t g a a t t t c g a t	948
O	y		813	c a c c t t g t g t g a c c a g c a a g g a a g t f g a t t t c t a c c c c a a c t a t c c g a t a c t a	872
D	b		949	c a c a t t c g t l c c a a g t c c g g c a a g t t g t g t t t c c c a a a g t c a t t t g c t c a c t a	1008
O	y		873	c c t a a g a c g t g t g t g t g a c t t c g c t c g t t t g g c a t a t g a t a g t a c a g c	932
D	b		1009	c g t a c c a c c t g t c t c t g t g t a t f c a t c g a a g c g c t g c c t t g a c t g c t g a c g	1068
O	y		933	t t t t g a a a c g t g a t g a a g t t a g t g c t t t a t g s g t g a t c c a a g g a a g a t a t g t t t g c	992
D	b		1069	c t t c a a g t c a a c g t a c t t c g g g c c a c c t g c t g a a g a c g r g	1114
O	y		993	t g a t c a g a t t c c a c c a c c a c t g y a g y g s a g a g a t c a a g g a t c a a g c a g c t g t t c a g	1052
D	b		1115	- - - - c g c t c t g c g c t g c t g c c t g c t g c t c c o g c g y g c a c g b a t c c a g t a a g	1170
O	y		1053	c t c t c t a a a g t t g t c c g g c t g t c c g t c t t t g g c g a g y g c c g t a a g c t g n a c a c t a	1112
D	b		1171	c g c c g t g t g t c t g a c a c t g c t a t b g c c g t g t t t g c c c t g c t g c a c a c t g t g t g c t g	1230
O	y		1113	c a t t g a a t a t g a a c t g c t g t g t c t g t c c t g c t g t g t g t g t t g t t g g c t g e t g a c a	1172
D	b		1231	c g t c t g t t t a a c a t t g t c a a g s g g a a g a t c a a g a a c a g a t c c a g a c t g c t g a g a t	1290
O	y		1173	c t g a t g a g c c t g a c t c t g t a c a g a t t g y g a a t a t a g a t c t t t g a c a g a a c a c a a	1232
D	b		1291	t g r g t g c t g c a g a a g c t g a g c c c g a c t g a g a c c c t a c t a c t t g t t g y c g a g	1350
O	y		1233	g a c a t c t c g a a a a a a c a g c t g s t g t a c a a c a c t a g a g a t a g s a t t g a c a c c c t a c a	1292
D	b		1351	a c c a g c c g a g g y g a a c a g c t c t g y c c a a g a t g a c a a c t g a a c a a c a a g a g y a g a c a a	1410
O	y		1293	g t t t a a c g g u c t g c t c a a g a g a t g y g a a g t g t g c c a g c a a g a a t t c t g t a c a t	1352
D	b		1411	c g g a a c g g g c t - - - - - g a a g c t g t a a g y c g g c c g t c g c t g c g a g c a g c t a c a t	1461
O	y		1353	c t c t c g t g t a t t t c a a t g a c a g c c a c c a c a g t g y g c t t t g g a a a t c g c c c	1412
D	b		1462	c a c t c c c t a c t t c g a c t c a g a c a g c c t a c a c a g c y g g c t t c g c a a g t g t c g c	1521
O	y		1413	a t c a c a g a c a t t g a a g a a g t c t t t g c a g t g c a t c a t a t a t g a t t g t c a t c t c t a	1472
D	b		1522	c a a a c g a a c a c t a g a a g a t c t t c t c a c t g c a a c a t g c t a c t a t c g g c c c t a t g c a	1581
O	y		1473	t g c a c a c a c t c t c g a a t t g a c g a c t a t t t c c a a g a t a g t a t g c a a a c a a c a a g	1582
D	b		1582	c g c g t g t g t c t c g g a a c g t a g c y c a t c a t c a c a g c g a t a c g c a t t c t	1611
O	y		1533	a t a c a t g a g a t g c t c a a c a g t t t c t g g a a c t c c t g a a g c t c t a a g c a g t g c a a a g	1592

Db	1642	gtaaccaagccgacacgacgcgacctcgtgcgacataatccgcgatccacccgtatccccagcc	1701
Qy	1593	attgagctgagcgagataatgataatattgtgtccactctgtgccatgtgccagagagcatlga	16522
Db	1702	ccctcaagcagcgatctgtgtgagtaattcttcacagcgccaccttggcggttgaaacaattgcatcga	1761
Qy	1653	cacagagaagctctcgtcagatactctgccccaagagacatgagaagccgacatactctgctgcaact	1712
Db	1762	caccacacgagctctcgtcagagcctcccttcagacgagctcgtcgcgacagacatcgccatgcaact	1821
Qy	1713	gaacgcgaaggtgttcaagagagacacccgcgctctccgctctgcccagtgatgtctgcctccg	1772
Db	1822	g - - - cacaagagaggtcccttcgaagcttgcgcgctgtttgagacagacgcgcgcgtgcgtcgcg	1878
Qy	1773	ggcactgcgcatactgagtlccacagacggtgacatctgtgcccagggagacctcaatccacatgc	18322
Db	1879	ggcactgctctcgtgcctctgcgcgcgcgcctctctgcagcgcggcgagagtaactcaatccacca	1938
Qy	1833	aggagagagcgtltgacacagcctctgccttctgtgttctctgtcctcccttgagaggtgacacaga	1892
Db	1939	aggcagtgccctgcagcgccctctacttgcctctgctcgtctccatgagaggtgcacgaagg	1998
Qy	1893	tgatgaggtctgtgcacatctctagaagaagagacgctgtttcgagagatgtgtctcggaagga	1952
Db	1999	tgacacacgtgcctgcacatccctaaaggagaggttgacatctgatatcgtctgtgagctgcgcccgcag	2058
Qy	1953	agccacaccttgcccagtlccctcgtgcgaatgtttaagcgccctgcacactgagatctgcagatg	2012
Db	2059	ggagcaggtctgtataaagcccaacgcgcgagtctgaaagggcgtcagatgacgtctccgcgcagtg	2118
Qy	2013	gatacaagcggatgcctctcagagaagaatgtctggaattctaaacgacctctccacatcctt	2072
Db	2119	tctgcagctcgtcgtcctctgcagacacgcctctgctctaccccgagtttgcccgcgctt	2178
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DT	30-NOV-1999 (first entry)	
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DE	Human potassium channel K+Hnov14 CDNA.	
XX		
KM	Potassium channel; ataxia; arrhythmia; epilepsy; Bartter's syndrome;	
KM	cardiovascular disorder; CNS disorder; renal disorder; ds.	
XX		
OS	Homo sapiens.	
XX		
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FT	variation	/product= "human K+Hnov14 potassium channel"
FT		replace (3168..7)
XX		/*tag= b
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PD	02-SEP-1999.	
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PF	22-FEB-1999;	99WO-US03826.
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PR	19-JAN-1999;	99US-0116448.
PR	25-FEB-1998;	98US-0076687.
PR	07-AUG-1998;	98US-0095836.
XX		
PA	(AXYS-) AXYS PHARM INC.	
XX		



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 QY 1596 gattgagcgaatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgat 1655  
 Db 1847 caagagcgcacgtcgtgagctacttccagccacgtcggtggaacaatgatgatgatgatgat 1906  
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 Db 2024 actgctctggtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 2083  
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 Db 2144 caccgtgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 2203  
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 Db 2324 tcgtggtcct 2332

RESULT 14  
 AA293334  
 ID AA293334 standard; CDNA: 3742 BP.  
 XX  
 AA293334:  
 04-JUL-2000 (first entry)  
 XX  
 DE Rat elK1 potassium channel gene.  
 XX  
 KW ElK1; elK2; eag1; eag2; erg1; potassium channel; membrane protein;  
 KW drug screening; hypertension; renal failure; diabetes insipidus;  
 KW diabetic nephropathy; hypothyroidism; goiter; hypoparathyroidism;  
 KW pancreatic insufficiency; diabetes mellitus; cystic fibrosis;  
 KW salivary; salivary insufficiency; diabetes mellitus; cystic fibrosis;  
 KW ion flux; transduction; signal transduction; assay; detection;  
 KW rat; ss.  
 XX  
 OS Rattus rattus.  
 XX  
 FH Key Location/Qualifiers  
 FT 53..3360  
 FT CDS  
 FT /tag= a  
 FT /product= ElK1 potassium channel protein  
 FT /note= Whilst this sequence is cross referenced to  
 FT a GENESBQ protein file, this nucleotide  
 FT sequence as it stands does not accurately  
 FT encode the protein contained within that  
 FT file. This sequence has been reproduced  
 FT accurately from the patent application

FT specification although for it to accurately  
 FT encode the protein described in GENESBQ  
 FT record AAY83028, it requires an Adenosine  
 FT nucleotide between nucleotide positions  
 FT 2048 and 2049 of this indexed sequence"

PN WO200012546-A1.  
 PD 09-MAR-2000.  
 XX  
 XX 31-AUG-1999; 99WO-US19902.  
 PE 31-AUG-1998; 98US-0098413.  
 PR (UYNV ) UNIV NEW YORK STATE RES FOUND.  
 PA McKinnon D, Dixon JE;  
 PI WPI: 2000-256585/22.  
 DR P-PSDB: AAY83028.  
 XX  
 XX Novel mammalian potassium channel genes and polypeptides encoded by  
 PT them for screening drugs useful for treating diseases such as  
 PT hypertension, acute renal failure, diabetes insipidus and  
 PT hypothyroidism -  
 PS Claim 1: Page 80-81; 102pp; English.

CC Potassium channel genes e.g. elK1, elK2 or eag2 are useful for  
 CC identifying modulators which are useful for treating hypertension,  
 CC acute and chronic renal failure, diabetes insipidus, diabetic  
 CC nephropathy, hyperthyroidism, goiter, hyperparathyroidism,  
 CC pancreatic insufficiency, diabetes mellitus, cystic fibrosis,  
 CC salivary insufficiency. The availability of the gene  
 CC sequences provides a tool for research into the physiological  
 CC characteristics of the various genes and proteins for potassium  
 CC channels including the development of medicines effective for  
 CC treating disease conditions associated with mutations or defects in  
 CC potassium channels and the screening of drugs to ensure that  
 CC potassium channels are not blocked or physiologically affected by  
 CC those drugs. The channel proteins encoded by these genes are also  
 CC useful themselves as reporter molecules in assay and detection  
 CC systems to measure changes in potassium concentration, membrane  
 CC potential, current flow, ion flux, transduction, signal  
 CC transduction, receptor-ligand interaction and second messenger  
 CC concentrations.  
 CC  
 CC Sequence 3742 BP; 1034 A; 903 C; 880 G; 925 T; 0 other;  
 XX  
 XX

Query Match 9.5%; Score 281.4; DB 21; Length 3742;  
 Best Local Similarity 50.4%; Pred. No. 1.2e-69;  
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 QY 75 caatg-----atactaatttgttgggaatgctca---gatagtgacgtgacctat 125  
 Db 118 cgacggaacacatagacacttccctcgtcgaacgtcccaagtgtgcaaaagtttcccat 177  
 QY 126 tgtgtacagcaatgatgatgttgcgaagctgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 185  
 Db 178 agtctactgttcagatgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 237  
 QY 186 aaaaagcagcagctgagtttatgtatggggagcagctgataagaacagctgataa 245  
 Db 238 gaagagtgagcagctgacagtttctgttggggagagcaacagcagcagctgagcttca 297  
 QY 246 agtcgagcaaacatttgagacatagtatgaattccttgaattctgtatgtacaagaa 305  
 Db 298 gatcgaagaagctcctgtgaggaagagtgatgttcaagaagaaatattgttctacaagaa 357

OY	306	gaacagagaaacctgctgctgttctctgtgtgaaatctgtccaatccgaacgaaacgagataa	365
Db	358	gaattggggtccatcttctgttgcctgttggatctgtctataaagaatgaaagagaga	417
OY	366	agtgatttatcttcttgacttctcagtgagataacg-----cttc	407
Db	418	tgtgtcccttctccgtgcccattccaaagataaacaagacgaagaatgaagatcttc	477
OY	408	caaacagccaattatgagatgatcatgtatgaaggctggtgggaagtcttctcggtcgacaag	467
Db	478	agaagaataaaaaagaagacagacgaacaaagaatcaagcgagggccacttcgctc	537
OY	468	agcacttgacaagcagcaggggtgtcctcgacgcagctgtgtccaaagctgtcaaaaagcga	527
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	588	ccaatgaagaagcagagcgaacaaagaactccctccatcatcatcttataatttgyttt	647
Db	652	agaagtataaggttcccgatgtcaaaaaaagctccaagttcatccctgtcgacttcagcaatt	711
OY	648	taagaacacgtgtggtatctgtgatactcttgatcttgaccttcataacagccaactgtgtccc	707
Db	712	taagctgtgctgtagctgtcatttctgtcgcaagcttttatgtgtgtgtgtgtgtgtcc	771
OY	708	ttataatgtctccttcaaaaacgcagcaat-----aatgttgctgtgctgtgtgt	758
Db	772	ttacaacgtgtgtcttcatcttgagcaatgaagatctctgtccacaactcgtgagcaaaagctcag	831
OY	759	tgatgatcatcgtggaatgattatcttcttgggtggacatgtgtcgaatttataaccactt	818
Db	832	tgacatcgtctgtggaatctctctctcatatagaatattatcttaattccgaacaaactta	891
OY	819	tgttggacaacagagggaggtgtgattctctgaacccaactatcatccgcaatgaactcctgaa	878
Db	892	tgtcagcaagctctgscgaaggtatcttggaaaggagatccatcttgatccatccactgtccac	951
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OY	1299	tgtgtctgtgtcctcaaggaaatgtggaaggtgtgtccacgaagaatctgtcttaactctctc	1358
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QY	1339	gtctatttcacaatagcaccgctccacagtgtyggctcttgggaacatcgcgccatccac	1418
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QY	1419	agacattgaagaagatcttgcagtgggcaatcatatgatattgggtccatctctcatggcac	1478
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QY	1479	catcttcgggaattgtagacatatttccacaagatlatatccacacacacacagatacca	1538
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QY	1539	tgaagctgtcaacagatgttcgggactctctgaagctccctacacaggtgcacaaagattgag	1598
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QY	1599	tgaaggaaatgatgttatatttgttccacttgttccatgtgtccagaagcatltgacacaga	1658
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QY	1719	caagatgttcaagaagacccgccttcgcgtgcgcagatgatgtgcgtccgcgggact	1778
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AC	AAZ50119;		
DT	04-MAY-2000	(first entry)	
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DE	Human Elk voltage gated potassium channel monomer encoding cDNA.		
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KM	Voltage gated potassium channel subunit; VGPCs; heLK; human; stroke;		
KM	Kv superfamily; Bag family; ether a go-go; Elk subfamily; modulator;		
KM	chromosome 12q13; resting potential; cell excitability; seizure;		
KM	CNS; migraine; psychotic; anticonvulsant; ion flux disorder; detection;		
KM	gene therapy; antimigrane; cerebroprotective; neuroprotective;		
KM	antipsychotic; ss.		
XX			
OS	Homo sapiens.		
XX			
PH	Key	Location/Qualifiers	
FT	mat_peptide	1..3249	
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FT		/product= "Human Elk polypeptide"	
FT		/note= "Alpha subunit of voltage gated potassium channel"	















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1  ? NAME/KEY: unsure
2  ? LOCATION: (1943)
3  ? OTHER INFORMATION: Unidentified at time of filing
4  ?
5  ? FEATURE:
6  ? NAME/KEY: unsure
7  ? LOCATION: (1971)
8  ? OTHER INFORMATION: Unidentified at time of filing
9  ?
10 ? FEATURE:
11 ? NAME/KEY: unsure
12 ? LOCATION: (1990)
13 ? OTHER INFORMATION: Unidentified at time of filing
14 ?
15 ? FEATURE:
16 ? NAME/KEY: unsure
17 ? LOCATION: (2001)
18 ? OTHER INFORMATION: Unidentified at time of filing
19 ?
20 ? FEATURE:
21 ? NAME/KEY: unsure
22 ? LOCATION: (2013)..(2019)
23 ? OTHER INFORMATION: Unidentified at time of filing
24 ?
25 ? FEATURE:
26 ? NAME/KEY: unsure
27 ? LOCATION: (3124)
28 ? OTHER INFORMATION: Unidentified at time of filing
29 ?
30 ? FEATURE:
31 ? NAME/KEY: unsure
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33 ? OTHER INFORMATION: Unidentified at time of filing
34 ?
35 ? FEATURE:
36 ? NAME/KEY: unsure
37 ? LOCATION: (3141)
38 ? OTHER INFORMATION: Unidentified at time of filing
39 ?
40 ? US-09-351-215-3

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Db	537	tttgaagactgcccgaactctctccgtcttctgtgcgctggcaggaanaacttggatcgatactc	596
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Db	557	agaatacggcgctgcgtcttcttaatgctctcctaagtgtcatctttgcctcgaaatgacacactg	656
OY	1176	gatgycctgcacatctgttgcacagcatctggggagctatcagaatctttgacagagacaccaagac	1235
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OY	1536	ccatgagatgtcacaacagtgtcttggaactctcgaagcctacacaggttgccaaagagtt	1595
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DB 5710 AGTCCCTGGGTGTGAAGCCAGACCTGCGCCGCCACCCAGACCAAGCCCATGAGAGG 5769  
QY 2543 aggac 2547  
DB 5770 AAAAC 5774

## RESULT 9

US-08-393-703-15  
Sequence 15, Application US/08393703  
Patent No. 5585239  
GENERAL INFORMATION:  
APPLICANT: Lamarco, Kelly  
APPLICANT: Wilson, Angus  
APPLICANT: Herr, Winship  
TITLE OF INVENTION: A NOVEL EKARYOTIC TRANSCRIPTION PROTEIN:  
TITLE OF INVENTION: HOST CELL FACTOR  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111-4187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/393,703  
FILING DATE: 24-FEB-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Osman, Richard A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: A-57503-2/RAO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 398-3249  
TELEX: 910 277299  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8252 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
PCT-08-393-703-15

Query Match 1.5%; Score 43.4; DB 1; Length 8252;  
Best Local Similarity 48.6%; Pred. No. 0.035;  
Matches 119; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

QY 2303 agggcaatgtctctacagagatgctccgcaacacagccctgtgaagcgccagcgctg 2362  
DB 5530 AAGAGCAATGGCTCATGAGCTGCGCGGACAGGTCCCGACACTGTGGCTCTGCTCCT 5589  
QY 2363 tcaccgtgctgagagatctctgcaagccgctatctctcagagcagctccacctccggg 2422  
DB 5590 CAACGGCCACTGAGACCGTGGCTCCATCCACACATTTGTGGCCGCCCAAGCGGTTGTGG 5649  
QY 2423 tgcacagacagcaagctacagcgccaggtgcgagtgcctgggcccacagggggcg 2482  
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QY 2543 aggac 2547

DB 5770 AAAAC 5774

## RESULT 10

PCT-US93-11721-15  
Sequence 15, Application PC/TUS9311721  
GENERAL INFORMATION:  
APPLICANT: Lamarco, Kelly  
APPLICANT: Wilson, Angus  
APPLICANT: Herr, Winship  
TITLE OF INVENTION: A NOVEL EKARYOTIC TRANSCRIPTION PROTEIN:  
TITLE OF INVENTION: HOST CELL FACTOR  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111-4187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/11721  
FILING DATE: 03-DEC-1993  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Osman, Richard A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: FP-57503-1/RAO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 398-3249  
TELEX: 910 277299  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8252 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
PCT-US93-11721-15

Query Match 1.5%; Score 43.4; DB 5; Length 8252;  
Best Local Similarity 48.6%; Pred. No. 0.035;  
Matches 119; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

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QY 2543 aggac 2547  
DB 5770 AAAAC 5774

[illegible]

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STREET: 419 Seventh Street, NW
City : Washington
STATE: DC
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DO$
SOFTWARE: Patentln Release #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,995
FILING DATE: 15-NOV-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/708,038
FILING DATE: 31-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, G. Kevin
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: SERRENO-2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEX: 202-737-3528
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..444
US-08-127-995-3

Query Match          1.4%      Score 40.2; DB 1; Length 444;
Best Local Similarity 54.4%; Pred: No. 0.039;
Matches   81; Conservative    0; Mismatches 68; Indels   0; Gaps   0

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Oy     2561 acattcccccgaagagcaaaaacyttcagycgaagccccacctgaagaagaacagactcgt 2640
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Db     268 GGCGTGATGCAGAACAGACCAAAGGGCAGTAGCTGGCAGTGTGGAGAAGACCAAAGTCGTGIG 327

Oy     2641 gacagtgcatcaccaagaagcgacttcgc 2669
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Db     328 GTCACTGGCAGCATTAACACACTCTTGGG 356


RESULT 13
US-08-764-343-2
Sequence 2, Application US/08764343
Patent No. 5739009
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPlicant: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL ADIPOCYTE-SPECIFIC
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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; NAME/KEY: CDS
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US-08-056-200-93

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Query Match 1.3%; Score 38.8; DB 1; Length 9551;
Best Local Similarity 53.2%; Pred. No. 0.94;
Matches 82; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

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 Job time: 20461 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 9, 2001, 03:01:29 : Search time 4156.91 Seconds

(without alignments)  
11774.884 Million cell updates/sec

Title: US-09-694-777-14

Perfect score: 2967

Sequence: 1 atgacatgctgctgggagcag.....gagacatttgcgagccagc 2967

Scoring table: IDENTITY\_NUC  
Gap 10.0, Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Minimum number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_da:\*  
2: gb\_hlg:\*  
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5: gb\_ov:\*  
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7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pl:\*  
10: gb\_ro:\*  
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14: gb\_vl:\*  
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17: em\_hum:\*  
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34: em\_or:\*  
35: em\_or:\*  
36: em\_or:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2967	100.0	2967	6	AX012972
2	2967	100.0	3083	6	AX012960
3	2967	100.0	3083	9	AF078742
4	2795	94.2	2886	6	AX012971
5	2795	94.2	3002	6	AX012959
6	2795	94.2	3002	6	AF078741
7	2791.8	94.1	3102	9	HSJ001366
8	2538.6	85.6	3486	4	BTEAG2
9	2442.2	82.3	4010	10	MM004294
10	2368.2	79.8	3405	4	BTEAG1
11	2255.8	76.0	4569	10	RNPCHS
12	1310	44.2	3507	10	RN0250280
13	1308.4	44.1	3374	10	AF185637
14	1294.4	43.6	3289	6	AF185637
15	856	28.9	153969	2	AL358977
16	617.2	20.8	4061	3	DROENG
17	543	18.3	3318	3	AF130443
18	477.8	16.1	14446	2	AL603791
19	477.8	16.1	150128	2	AL590132
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21	340	11.5	3352	9	AF311913
22	339.2	11.4	3480	6	AR139486
23	339.2	11.4	3950	6	AR139487
24	339.2	11.4	4070	6	HSU04270
25	339.2	11.4	4070	11	G31722
26	337.2	11.4	3898	4	CEA243344
27	336.6	11.3	3820	4	OCU87513
28	327.6	11.0	3889	10	RN26106
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30	326	11.0	3150	10	AF012869
31	326	11.0	4235	10	AF012868
32	283.2	9.5	3807	10	AF016191
33	281.4	9.5	3743	10	AF061957
34	281.2	9.5	3610	9	AB022696
35	280	9.4	4113	5	AF032897
36	279.8	9.4	1581	9	GGA271210
37	279.6	9.4	3853	10	AB033108
38	278	9.4	3252	6	AX027893
39	275.2	9.3	3629	10	MM0291608
40	272.8	9.2	3142	6	AR087492
41	272.8	9.2	3142	6	AR103880
42	271	9.1	36818	3	AF036695
43	271	9.1	317781	2	AC006906
44	270	9.1	2819	9	BC001914
45	269.6	9.1	3337	9	AB044806

## ALIGNMENTS

RESULT 1  
LOCUS AX012972 2967 bp DNA  
DEFINITION Sequence 14 from Patent WO954463.  
ACCESSION AX012972  
VERSION AX012972.1 GI:10040220  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 (bases 1 to 2967)  
Sanchez, P.A., Beckh, S., Stuehmer, W., Brueggemann, A.,  
Pardo-Fernandez, L.A., Weseloh, R. and Del Camino  
Fernandez-Miranda, D.  
Human k<-> ion channel and therapeutic applications thereof  
Patent: WO 9934463-A 14 28-OCT-1999;  
MAX PLANC GESELLSCHAFT (DE); SANCHEZ PEREZ ARACELI (DE); BECKH  
SYNOEVE (DE); STUEHMER WALTER (DE); BRUEGEMANN ANDREA (DE); PARDO  
FERNANDEZ LUIS ANGEL (DE); WESELOH RUDIGER (DE); DEL CAMINO

TITLE JOURNAL  
AX012972 2967 bp DNA  
Sequence 14 from Patent WO954463.  
AX012972.1 GI:10040220  
07-SEP-2000

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AUTHORS Pardo, L.A., del Camino, D., Sanchez, A., Alves, F., Bruggemann, A.,  
Beck, S. and Stuhmer, W.  
TITLE Oncogenic potential of EAG K(+) channels  
JOURNAL EMBO J. 18 (20), 5540-5547 (1999)  
MEDLINE 99452761  
REFERENCE 2 (bases 1 to 3083)  
AUTHORS Pardo, L.A., del Camino, D., Sanchez, A., Beck, S. and Stuhmer, W.  
DIRECT SUBMISSION Submitted (17-JUL-1998) MBNS, MPI exp. Medizin, Hermann-Rein-Str.  
JOURNAL 3, Göttingen D37075, Germany  
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LOCUS AF078741 Homo sapiens voltage-gated potassium channel eag (EAG) mRNA,  
DEFINITION complete cds.  
ACCESSION AF078741 GI:3790562  
VERSION AF078741.1  
KEYWORDS human.  
SOURCE  
ORGANISM Homo sapiens  
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Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 3002)  
Pardo, L.A., del Camino, D., Sanchez, A., Alves, F., Bruggemann, A.,  
Beckh, S. and Stuhmer, W.  
Oncogenic potential of EAG K(+) channels  
EMBO J. 18 (20), 5540-5547 (1999)  
99452761  
JOURNAL 2 (bases 1 to 3002)  
MEDLINE Pardo, L.A., del Camino, D., Sanchez, A., Beckh, S. and Stuhmer, W.  
REFERENCE Direct Submission  
AUTHORS Submitted (17-JUN-1998) MBNS, MPI exp. Medizin, Hermann-Rein-Str.  
JOURNAL 3, Göttingen D37075, Germany  
LOCATION/Qualifiers  
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BASE COUNT 748 a 751 c 825 g 678 t  
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DEFINITION	Homo sapiens potassium channel h-eag.				
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REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.				
TITLE	1 (bases 1 to 3102)				
JOURNAL	Occiodoro, T.				
	Direct Submission				
	Submitted (02-OCT-1997)				
	Occhiodoro T., Department of Physiology,				
	Centrale Medical Universitaire, 1 Rue Michel Servet, Geneva 1211,				

REFERENCE 2 (bases 1 to 3102)  
Ochiodoro, T., Bernheim, L., Liu, J. H., Bijlenga, P., Sinnreich, M.,  
AUTHORS Bader, C. R. and Fischer-Loughned, J.  
TITLE Cloning of a human ether-a-go-go potassium channel expressed in  
myoblasts at the onset of fusion  
JOURNAL FEBS Lett. 434 (1-2), 177-182 (1998)  
MEDLINE 98408853  
FEATURES

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1. 3102  
Location/Qualifiers

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Query Match 94.1%; Score 2791.8; DB 9; Length 3102;  
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RESULT	8		
LOCUS	BTFAG2	3486 bp	MAN
DEFINITION	Bos taurus mRNA for EAG-channel, splice variant.		09-JUL-1998
ACCESSION	U13431		
VERSION	U13431.1	GI:2584732	
KEYWORDS	EAG channel; eag2 gene; K+ channel.		
SOURCE	cow.		
ORGANISM	Bos taurus		
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	1 (bases 1 to 3486)		
	Frings,S., Bull,N., Dzeja,C., Angele,A., Hagen,V., Kaupp,U.B. and Baumann,A.		
REFERENCE	Characterization of ether-a-go-go channels present in photoreceptors reveals similarity to Ix, a K+ current in rod inner segments		
AUTHORS	J. Gen. Physiol. 111 (4), 583-599 (1998)		
JOURNAL	98190099		
MEDLINE	2 (bases 1 to 3486)		
REFERENCE	Baumann,A.		
AUTHORS	Direct Submission		
TITLE	Submitted (28-MAY-1997) A. Baumann, Institut fuer Biologische Informationsverarbeitung, Forschungszentrum Juelich, P.O.Box 1913,		
JOURNAL	52425 Juelich, FRG		
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LOCUS MMU04294 4010 bp mRNA 28-FEB-1995  
DEFINITION Mus musculus potassium channel subunit (m-eag) mRNA, complete cds.  
ACCESSION U04294  
VERSION U04294.1 GI:487739  
KEYWORDS house mouse.  
SOURCE Mus musculus  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 114 to 3083)  
AUTHORS Warmke,J.W. and Ganetzky,B.  
TITLE A family of potassium channel genes related to eag in Drosophila and mammals  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 91 (8), 3438-3442 (1994)  
MEDLINE 94211879  
REFERENCE 2 (bases 1 to 4010)  
AUTHORS Warmke,J.W.  
TITLE Direct Submission  
JOURNAL Submitted (10-DEC-1993) Jeffrey W. Warmke, Genetics and Molecular Biology, Merck Research Laboratories, 126 East Lincoln Avenue, P.O. Box 2000, Rahway, NJ 07065, USA  
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DEFINITION	R.norvegicus mRNA for potassium channel subunit.		
ACCESSION	Z34264		
VERSION	Z34264.1 GI:557264		
KEYWORDS	K+ channel; K+ channel protein; potassium channel.		
SOURCE	Norway rat.		
ORGANISM	Rattus norvegicus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Ratus.		
REFERENCE	1 (bases 1 to 4569)		
AUTHORS	Ludwig,J., Terlau,H., Wunder,F., Bruggemann,A., Pardo,L.A., Marquardt,A., Stuhmer,W. and Pongs,O. Functional expression of a rat homologue of the voltage gated either a go-go potassium channel reveals differences in selectivity and activation kinetics between the Drosophila channel and its mammalian counterpart		
TITLE	EMBO J. 13 (19), 4451-4458 (1994)		
JOURNAL	95009946		
MEDLINE	2 (bases 1 to 4569)		
REFERENCE	Ludwig,J.		
AUTHORS	Direct Submission		
TITLE	Submitted (06-JUN-1994) Ludwig J, ZMNH, Institut fuer neurale Signalverarbeitung, Martinistr. 52, Hamburg, FRG, D-20251		
JOURNAL	Location/Qualifiers		
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TITLE	/clone="pregn"		
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REFERENCE	/clone_lib="rat cerebellum cDNA-library from F. Mestieux"		
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TITLE	/standard_name="K channel"		
JOURNAL	/evidence-experimental		
MEDLINE	/product="potassium channel subunit"		
REFERENCE	210. 3098		
AUTHORS	/standard_name="K channel"		
TITLE	/codon_start=1		
JOURNAL	/evidence-experimental		
MEDLINE	/product="potassium channel subunit"		
REFERENCE	/protein_id="CAA84018.1"		
AUTHORS	/db_xref="GI:557265"		
TITLE	/db_xref="SPTRMBL:063472"		
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[illegible]









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DEFINITION Rattus norvegicus potassium channel Eag2 (Eag2) mRNA, complete cds.  
ACCESSION AF185637  
VERSION AF185637.1 GI:6625693  
KEYWORDS  
SOURCE  
ORGANISM Norway rat.  
Rattus norvegicus  
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
REFERENCE 1 (bases 1 to 3374)  
AUTHORS Saganich,M.J., Vega-Saenz de Miera,E., Nadal,M.S., Baker,H.,  
Coetzee,W.A. and Rudy,B.  
TITLE Cloning of components of a novel subthreshold-activating K(+) channel with a unique pattern of expression in the cerebral cortex  
JOURNAL J. Neurosci. 19 (24), 10789-10802 (1999)  
MEDLINE 20063035  
REFERENCE 2 (bases 1 to 3374)  
AUTHORS Saganich,M.J., Vega-Saenz de Miera,E., Nadal,M.S., Baker,H.,  
Coetzee,W.A. and Rudy,B.  
TITLE Direct Submission  
JOURNAL Submitted (13-SEP-1999) Physiology and Neurosciences, New York University School of Medicine, 550 First Avenue, New York, NY 10016, USA



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 Oy 787 gttgacatgtgtcctaatttccatcacaccttgtgtgtgtgtgtgtgtgtgtgtgtgtgt 846  
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 Oy 967 gttgtatccaggaagattgt 1026  
 Db 966 ----- 965  
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 Db 966 ----AGGAATTCAGACGCTCTTCAAGTCTTTAAAGTGGTGGCTCTTACGACTGGGC 1021  
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 Db 1022 CGGTGTGGCTTGAAGAACTGACATTTACCTTGAATATGAGACAGACAGTCTCTGTCTCTG 1081  
 Oy 1147 gttgt 1206  
 Db 1147 gttgt 1206

Db 1082 GTGTGTGTGTTTGACATGTTGGCCCACTGGCTGAGCTGATATGATATGATCGGAGAC 1141  
 Oy 1207 tatgagatcttgcagcaggaacccaagacaatccgcaacaagcgtgtgttaccacta 1266  
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 Oy 1327 gtcaccaagaatcttgccttccatccctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1386  
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 Oy 1387 agt 1446  
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 Db 1379 ATGAT 1438  
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 Db 1619 ATGAGAGCTGATATGTGTGTATCTTAACCGGAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1678  
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.7e-207;  
Matches 856; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 26611 GAATGAGGCCCCCTGTGATCTTGCCCCGGACCACCTGTCTCGGCGCTTTCAGAGATT 26552  
QY 2232 ccgacacagaagaagccagctgcagctgaagagaagggccggagacctgaatgacct 2291  
DB 26551 CCGACACAGAAAGAGCCAGCGCTGGCAGCTGAGAGAGGGGGCCGGAGCTGGATGACCT 26492  
QY 2292 agatgtgagaagggcaatgtctcttaacagagcatgtcctccgccaacacagcctctgaa 2351  
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DB 26431 GGCAGCGGTGTCACTGTGCTGAGAGTCCAGCCGCCCTATCTTTCAGGCAGCCCTC 26372  
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DB 26371 CACTCTCGGGGTGCCAACCACGCAAGCTACAGGGCCAGGTTCCGAGTGGTGGGCC 26312  
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QY 2532 cgggaagaagtgaagactgtgaacaaagtgtccaaggtcgtgtagtgagacactccga 2591  
DB 26251 CGGGAAGAGTGAGAGCTGGAACAAGTGTCCAAAGCTGAGTGAAGACACTTCCCGA 26192  
QY 2592 gagaacaaagcgtcgaagcgaagccacactgaagaagaacagactcgtgtgaacagtgcac 2651  
DB 26191 GAGGACAAAGCGTTCAGGCGAGGCCACACTGAAGAGACAGACTGCTGACAGTGGCAT 26132  
QY 2652 caccagaagcgaactgtgccttgacaacgltgggtgaagccagagttccccaagatcgag 2711  
DB 26131 CACCAAGAGGACTTGGGCTGGACAACGTGGTGAAGGCCAGAGTCCCAAGATCGAG 26072  
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QY 2832 gaccaaatgaagaacagctctctgagatactcagagataataactccagaagaatcctc 2891  
DB 25951 GACCAATATGTAGAAACAGCTCTGTGATTAAGATATTAACCTTCCAGAAATCTCTC 25892  
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QY 2952 catttttgagccagc 2967  
DB 25831 CATTTTTGAGCCAGC 25816

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2M nucleic - nucleic search, using sw model

Run on: December 9, 2001, 02:58:14 ; Search time 2450.64 Seconds  
(without alignments)  
13009.959 Million cell updates/sec

Title: US-09-694-777-14

Perfect score: 2967

Sequence: 1 atgacacatgctgggggagcag.....gagacatttggagcagc 2967

Scoring table: IDENTITY\_NUC

Gapop 10.0, Gapept 1.0

Searched: 11351937 seqs, 537289281 residues

Minimal number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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4: em\_estom:\*  
5: em\_estpl:\*  
6: em\_estba:\*  
7: em\_estro:\*  
8: em\_estov:\*  
9: em\_hic:\*  
10: qb\_est1:\*  
11: qb\_est2:\*  
12: qb\_hic:\*  
13: qb\_gss:\*  
14: em\_gss\_fun:\*  
15: em\_gss\_hum:\*  
16: em\_gss\_inv:\*  
17: em\_gss\_pln:\*  
18: em\_gss\_pro:\*  
19: em\_gss\_pro:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	430	14.5	1706	11 U69185	U69185 U69185 Soar
2	374.6	12.6	908	13 CNS0390G	AL233305 Tetradon
3	353.2	11.9	452	11 BF949480	BF949480 MR3-NM21
4	288	9.7	1007	13 CNS0422N	AL270968 Tetradon
5	270.8	9.1	1100	13 CNS055QL	AL352182 Tetradon
6	259.4	8.7	806	13 CNS04PL9	AL301446 Tetradon
7	258	8.7	945	13 CNS03A41	AL234730 Tetradon
8	202.2	6.8	557	11 B1134074	B1134074 UI-M-BH3-
9	199.6	6.7	308	11 F05455	F05455 HSC08R081 n
10	197.4	6.7	372	10 BB315626	BB315626 BB315626
11	196.4	6.6	315	10 BB317367	BB317367 BB317367
12	193.8	6.5	294	10 BB318360	BB318360 BB318360

13	193.8	6.5	1096	11 BF347563	BF347563 602020415
14	192	6.5	860	13 CNS02091	AL175311 Tetradon
15	189	6.4	414	10 AU169146	AU169146 AU169146
16	188.6	6.4	293	10 BB319507	BB319507 BB319507
17	180.2	6.1	1120	13 CNS02N8E	AL205079 Tetradon
18	177.8	6.0	281	11 F05456	F05456 HSC08F091 n
19	176.4	5.9	791	11 AU0840193	AU0840193 AU0840193
20	168.8	5.7	760	13 CNS0343V	AL243796 Tetradon
21	164	5.5	850	13 CNS03MKD	AL263830 Tetradon
22	161	5.4	1063	13 CNS0422O	AL270969 Tetradon
23	160	5.4	803	10 BE382810	BE382810 601297818
24	159.4	5.4	926	11 BF315250	BF315250 601899133
25	158.2	5.3	1048	13 CNS02BPD	AL190160 Tetradon
26	156.6	5.3	884	11 BF311665	BF311665 601897141
27	156.6	5.3	1101	13 CNS05AWH	AL329066 Tetradon
28	156.2	5.3	769	13 CNS04KEY	AL294739 Tetradon
29	155.2	5.2	365	10 BB314638	BB314638 BB314638
30	153	5.2	816	13 CNS02XOV	AL217768 Tetradon
31	150.6	5.1	282	10 BB315188	BB315188 BB315188
32	150.4	5.1	501	11 B1341020	B1341020 368212 MA
33	150.2	5.1	914	13 CNS03WKE	AL263831 Tetradon
34	146.2	4.9	240	10 BB312893	BB312893 BB312893
35	145.8	4.9	853	13 CNS03QSO	AL263533 Tetradon
36	144.4	4.9	1013	13 CNS0511Y	AL316303 Tetradon
37	140.4	4.7	464	10 AM886063	AM886063 RC6-OT007
38	138	4.7	1036	13 CNS0020R	AL061908 Drosophila
39	137.6	4.6	424	10 A1272282	A1272282 ap23C04.x
40	136.8	4.6	501	10 AW249298	AW249298 2821074.5
41	134	4.5	716	13 CNS04ABX	AL281562 Tetradon
42	132.8	4.5	1084	13 CNS057J2	AL334695 Tetradon
43	131.2	4.4	480	11 R55596	R55596 Y988F08.r1
44	129.8	4.4	893	11 BF317069	BF317069 601903465
45	128.2	4.3	910	13 CNS0328B	AL224516 Tetradon

#### ALIGNMENTS

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LOCUS U69185 1706 bp mRNA EST 27-OCT-1999  
DEFINITION U69185 Soares infant brain INIB Homo sapiens CDNA clone c-b0f09,  
mRNA sequence.  
ACCESSION U69185  
VERSION U69185.1 GI:2739409  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (bases 1 to 1706)  
AUTHORS G., Ballabio, A. and Zollo, M., Cucciarli, M., Banfi, S., Borsani  
Volorio, S., Simon, G., Repetto, M., Zollo, M., Cucciarli, M., Banfi, S., Borsani  
TITLE Sequencing analysis of forty-eight human image cDNA clones similar  
to drosophila mutant protein  
JOURNAL DNA Seq. 9 (5-6), 307-315 (1998)  
MEDLINE 99452388  
COMMENT Contact: Zollo, Massimo  
Telethon Institute of Genetics and Medicine  
Via Olgettina 58, Milan, MI 20132, Italy  
Email: zollo@tigem.it.  
FEATURES  
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/db\_xref="taxon:9606"  
/clone="c-b0f09"  
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/sex="female"  
/dev\_stage="73 days post natal"  
/lab\_host="DH10B (ampicillin resistant)"  
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I; Site\_2: Hind III; 1st strand cDNA was primed with a Not  
I - oligo(dT) primer [5'







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Db	126	TGATTCATGTAAAGGCTGGCGGGAAGTTTGCTCGCTGCACAGAGCACTGCACAAGACGA	67	
Oy	485	gggggtgtctgcacgaagctgcctccaaagctgcacaaaaggc	526	
Db	66	GGGGTGTCTGCACAGACT-GCTCCAAGCGTGCACAAAAAGGG	26	
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LOCUS		CNS0422N		GSS
DEFINITION		Tetraodon nigroviridis genome survey sequence T7 end of clone 075H21 of library G from Tetraodon nigroviridis, genomic survey sequence.		18-MAY-2000
ACCESSION		AL270968	GI:7992916	
SOURCE		GSS; genome survey sequence.		
ORGANISM		Tetraodon nigroviridis		
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostei; Acanthomorpha; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Tetraodontidae; Tetraodon.		
AUTHORS		1 (bases 1 to 1007) Roest-Crolius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.		
TITLE		Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis		
JOURNAL		Unpublished		
REFERENCE		2 (bases 1 to 1007)		
AUTHORS		Roest-Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.		
TITLE		Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence		
JOURNAL		Unpublished		
REFERENCE		3 (bases 1 to 1007)		
AUTHORS		Genoscope.		
TITLE		Direct Submission		
JOURNAL		Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases		
COMMENT		This sequence is a single read and was generated as part of a large scale clone-and-sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.		
FEATURES		Location/Qualifiers		
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Query Match		9.7%; Score 288; DB 13; Length 1007;		
Best Local Similarity		66.1%; Pred. No. 2,7e-65;		
Matches 481; Conservative		0; Mismatches 185; Indels 62; Gaps 2;		
Db	8	CCACCTTTGTGGGCCCGCGGGGAGGTCAATTCGACCACCAAGCTATTCGCACCAACT	67	
Oy	872	acctgaagacgtgttgttgattgaccttctgtctgtttgcatatgatgtlcatcaacy	931	
Db	68	ACGTCAGAGACCTGGTTCATCATGCATCGCTGCTGCTGCCCTATGACGTCAATCAACG	127	
Oy	932	ctttgagaacgtgatgatgagtgatgctccttatgg-----gtatgcc	974	

[illegible]

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LOCUS	
DEFINITION	CNS04PL9 806 bp DNA GSS 24-MAY-2000 Tetraodon nigroviridis genome survey sequence pUC-ori end of clone 127B02 of library G from Tetraodon nigroviridis, genomic survey sequence.
ACCESSION	AL301446
VERSION	AL301446.1 GI:8178499
KEYWORDS	GSS: genome survey sequence.
SOURCE	Tetraodon nigroviridis.
ORGANISM	Tetraodon nigroviridis Euteleostei: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Actinopterygii: Neopterygii: Teleostei: Euteleostei: Neoteleostei: Acanthopterygii: Acanthopterygii: Percomorpha: Tetraodontiformes; Tetraodontidae: Tetraodon. 1 (bases 1 to 806)
REFERENCE	Rost-Crollius,H., Jallion,O., Dasilva,C., Fizames,C., Fisher,C., Bonneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
AUTHORS	

RESULT	7
CNS03A41/c	
LOCUS	CNS03A41
DEFINITION	945 bp DNA GSS 15-MAY-2000 Tetradon nigroviridis genome survey sequence T7 end of clone 008J12 of library G from Tetradon nigroviridis, genomic survey

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ACCESSION sequence.
AL234730.1 GI:7893865
KEYWORDS CSS: genome survey sequence.
SOURCE Tetraodon nigroviridis.
ORGANISM Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
REFERENCE 1 (bases 1 to 945)
AUTHORS Roest-Crollius,H., Jaillon,O., Dasilva,C., Fitzames,C., Fisher,C.,
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Weissenbach,J.
TITLE Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 945)
AUTHORS Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fitzames,C., Wincker,P., Brothier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
TITLE Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 945)
AUTHORS Direct Submission
COMMENT Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
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Matches 508; Conservative 2; Mismatches 142; Indels 146; Gaps 2;
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DB 896 CGGTGCTCTACGCCACMAATTTTCGGAACGACACACATCTCCAGAGATGACACA 837
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DB 836 ACACACACCGCTACCGACGATGCTCAACAACGTCGCGACTTCTCAAGCTCTACGAG 777
QY 1583 tgcacaagaagatgagtgagagtaatgataatgcttcacactggtctccatgca 1642
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DB 656 TGTCCTGAGGTCTTCTCTCTGCTCAGGTCTCTCCATTCTTCMAAAGACATGGCGGG 597
QY 1696 gacatcgcgtgacccggaacagtgctcaaggaacccggcctccgcgtgagcc 1755
DB 596 GACATCTGCGTCCACCTCAACAGGAGGTCTTCAACGACACCGGCTTCCGCTGGGCC 537
QY 1756 agtgaatgctgctcctcgagacatgagatctccagacggtgactgtgccccaggg 1815

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DB 536 AGCGACGGCTGCTGCTCTCTGCGCTGAGCTTCACAGACACTGACGCCGCCGCCG 477
QY 1816 gaccatcatcacatcagagagagcgttgacagcctctgcttgcttgcttcgc 1875
DB 476 GACCTCATCTTCCACCTCGGGGAGAGACGTGAGACACCTCTGCTTGTGCTGGGCTCC 417
QY 1876 ctgagagtgatcaagaatgatgagtggtgagcatct----- 1913
DB 416 CTCGAAGTATCAGACGACGAGGATGATGCGCATCTCTCGTAAACAGCAGCAAGCA 357
QY 1914 -----agg 1916
DB 356 GTGTGCGACCCGCTTCTGTATTTTGGCCGTGACGCGGGGTTTGGCCGCCAGCAG 297
QY 1917 aaagagagacgttgatgagatgcttcggaaggaagcacccttcgcagctcgtgc 1976
DB 296 CAAGGGGACGCTTTTGGGACGCTCTTGTGGAAGGAGAGACACCTGCGCAGGCTCGCC 237
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DB 236 CAACGTGCGGCGGCTGACCTGACCTGACGACGTCATCAGAGAGGAGGCGCTGATGA 177
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QY 2097 caacttgaggaagagat 2114
DB 116 CAACCTACGCCAAGCGGT 99
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DEFINITION UI-M-BH3-bsh-d-08-0-UI.s1 NIH_BMAP_M.S4 Mus musculus cDNA clone
VERSION B1134074
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 557)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: MEST@mail.nih.gov
Oligo-dT track not found. Not 1 site shown in beginning of sequence
is likely internal to the message. cDNA library preparation: M.B.
Soares Lab Clone distribution: Researchers may obtain BMAP cDNA
clones from RESEARCH GENERAL. It should be noted that Bento Soares
is generating a small number of additional specialized
non-redundant arrays of BMAP cDNAs whose availability will be
considered under appropriate and limited collaborative arrangements
Seq primer: M13 Forward
POLYA-NO.
FEATURES
source
1..557
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UI-M-BH3-bsh-d-08-0-UI"
/clone_1lb="NIH_BMAP_M.S4"
/dev_stage="27-32 days"

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TITLE  
JOURNAL  
COMMENT

Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,I., Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tomioka,N., Toya,T., Tsunoda,Y., Watanabe,A., Watanabe,S., Yamamura,T., Yamanaoka,I., Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.  
RIKEN Mouse ESTs (Konno,H., et al.)  
Unpublished (2000)  
Contact: Yoshihide Hayashizaki  
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The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-resgsc.riken.go.jp,  
URL: http://genome.gsc.riken.go.jp/  
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
Thermostabilization and thermocatalytic activation of thermostable enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)  
Itoh,M., Kitsuai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.  
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)  
Carninci,P. and Hayashizaki,Y.  
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)  
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.

FEATURES  
source

Location/Qualifiers  
1. 315  
/organism="Mus musculus"  
/db\_xref="taxon:10090"  
/clone\_lib="B230369B17"  
/clone\_lib="RIKEN full-length enriched, adult male corpora quadrigenima"  
/sex="male"  
/tissue\_type="corpora quadrigenima"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/note="Site\_1: SalI; Site\_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGATCCAGAGCTTTTCTTTTCTTTTCTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGATCCAGAGCTTTTCTTTTCTTTTCTTTVN 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FIC I."

BASE COUNT  
ORIGIN

89 a 93 c 66 g 67 t

Query Match 6.6%; Score 196.4; DB 10; Length 315;  
Best local Similarity 80.4%; Pred. No. 3.7e-41;  
Matches 230; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

OY 2682 ggggtgagccagagatcccgatgagatccatctcgcaaggtcgaagcattcgt 2741  
DB 5 GGGTGAAGACCATATTCATGACCGACCCCATTTAGCTGAGATCAACATTTCTTT 64

OY 2742 ctaccatcccttgagcagagctgcagagccacagctcctggaagctgagcagagctgaa 2801  
DB 65 CTACCCCATCTCTGACACAGACCTCTGAGGCGCAGCTGCGAGAGTAAATATGAGCTGAA 124  
OY 2802 ggaagacatcaagagcttaaacgccaataatgacatattggaacagctcctgagat 2861  
DB 125 GGAGATTTTCAAGCCCTTGAATCCCAATGACCTCATTTGGAAGACCTTTCTGAGAT 184  
OY 2862 actcagatattactcctcagaagatcctcagctcctcctcagagctgtttgaaatc 2921  
DB 185 ACTCAGATTAATTAATTTCCAGAGGCTCCGCCCAATCTCTCAGAGAGACGATGATCTC 244  
OY 2922 gaggcagatcccaagcagagcagagacatttttgagcagc 2967  
DB 245 CAGCCCGACGTCCTCAGATTCAGACAGACATTTTGGAGCAAGC 290

RESULT 12  
LOCUS BB318360 294 bp mRNA EST 11-JUL-2000  
DEFINITION BB318360 RIKEN full-length enriched, adult male corpora quadrigenima Mus musculus cDNA clone B230374110 3' similar to U04294 Mus musculus potassium channel subunit (m-eag) mRNA, mRNA sequence.  
ACCESSION BB318360  
VERSION BB318360.1 GI:9025395  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus.

REFERENCE  
AUTHORS  
Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusabae,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A., Watanabe,S., Yamamura,T., Yamaoka,I., Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.  
RIKEN Mouse ESTs (Konno,H., et al.)  
Unpublished (2000)  
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The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-resgsc.riken.go.jp,  
URL: http://genome.gsc.riken.go.jp/  
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
Thermostabilization and thermocatalytic activation of thermostable enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)  
Itoh,M., Kitsuai,T., Akiyama,J., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.  
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)  
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High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)  
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TITLE  
JOURNAL  
COMMENTFEATURES  
source

Location/Qualifiers  
1. 294  
/organism="Mus musculus"



DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone 222E23 of library 6 from Tetraodon nigroviridis, genomic survey sequence.

ACCESSION AL175311.1 GI:7813368

VERSION AL175311.1

KEYWORDS GSS: genome survey sequence.

SOURCE Tetraodon nigroviridis.

ORGANISM Tetraodon nigroviridis

REFERENCE 1 (bases 1 to 800) Roest-Crolius, H., Jaillon, O., Dasilva, C., Fizes, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissbach, J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis

TITLE Unpublished

JOURNAL 2 (bases 1 to 800)

REFERENCE Roest-Crolius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizes, C., Wincker, P., Brothier, P., Quetier, F., Saurin, W. and Weissbach, J. Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence

TITLE Unpublished

JOURNAL 3 (bases 1 to 800)

REFERENCE Genoscope.

AUTHORS Direct Submission

TITLE Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases

JOURNAL This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/Tetraodon>.

COMMENT Location/Qualifiers

FEATURES

source 1..800

/organism="Tetraodon nigroviridis"

/db\_xref="taxon:99883"

/clone="222E23"

/clone\_1lb="G"

/note="Genoscope sequence ID : CONG222AC12LP1-end : 77"

BASE COUNT 187 a 206 c 198 g 201 t 8 others

ORIGIN

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Best Local Similarity 83.7%; Pred. No. 7.8e-40;

Matches 216; Conservative 1; Mismatches 41; Indels 0; Gaps 0;

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56 AGGTGCTGACATTTGTCCTCCAAAGACATGAGAGCGGACATTTGTTACCTCAACCCCA 115

1721 aggtgttcaagagacaccgccttcgcgtcgtgcacgtgatgctgcctccggagactgg 1780

116 AAGTTTCAAGAGACACCGCGGCTTCGCGTCGCGACGAGCGGCTGCTCCGAGCGGTGG 175

1781 ccatgagagttccaaagcgtgactgtgcccagggagactcatctaccatgcagagaga 1840

176 CCATGGGGTTCCAAACATGCACGCGCCCGCGGACCTATCTACACCGCGCGAGGA 235

1841 gcggtgacagcctcgtgtgttctgcctccctgagagtgatgcacaaagatgagagg 1900

236 GCGTGGACAGCGCTGTGTTTGTGCTGGGGTCCCTGAGAGTCAATCCAGATGACGAGG 295

1901 tgggtgcacatctagaa 1918

296 TGGTGGCATTTTAGTA 313

RESULT 15

AUI69146 414 bp mRNA EST 29-JAN-2001

LOCUS

DEFINITION AUI69146 01-br-ad cDNA Oryzias latipes cDNA clone br4239, mRNA sequence.

ACCESSION AUI69146

VERSION AUI69146.1 GI:12591215

KEYWORDS EST.

SOURCE Japanese medaka.

ORGANISM Oryzias latipes

REFERENCE 1 (bases 1 to 414) Mita, K., Ishikawa, Y. and Yamauchi, M. Establishment of cDNA database of medaka, Oryzias latipes

AUTHORS Unpublished (2001)

TITLE Contact: Mita K

JOURNAL Genome Research Group

COMMENT National Institute of Radiological Sciences

Unpublished (2001)

Genome Research Group

Yamauchi, M. and Ishikawa, Y. Chiba 263-8555, Japan

Email: kmitsuen@nirs.go.jp

method: uni-directional sequence direction: sequenced from T3 primer (5' -> 3')

FEATURES

source 1..414

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/strain="HNI"

/db\_xref="taxon:8090"

/clone="br4239"

/clone\_1lb="01-br-ad cDNA"

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/dev\_stage="adult"

BASE COUNT 133 a 86 c 92 g 101 t 2 others

ORIGIN

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Best Local Similarity 79.6%; Pred. No. 3.8e-39;

Matches 222; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

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15 CCTCAGNAACACCTTCCTCGNAAACATGCTCGCGCTCAACGATACAAATTTGTGC 74

95 tgggaatgctcagatagtgactggtcctatgtgtgacagcaatgagatlttgcaagc 154

75 TGGGAATGCTCAGATGTGGAGCTGCGCAATGTCTACGACGACGATGGCTCTCGCAAC 134

155 tgtctggtatcacagggagagatgagcaaaaaagcagacctgcagtttatgtatg 214

135 TCTCTGTTACCATCGAGCTGAGGTCATGCAGAGACGACACATGCACTTTATGTATG 194

215 gggagctgactgataaagcagatgtaaaagtgtggcggaacatttggactatgaga 274

195 GAGAGCTGCAACAGAGGACACGAGAAAGTGGCGCTGCTTTGAGAAATTATGAGA 254

275 tgaattccttgaattctgactgataaagaaagaaagaaagaaagaaagaaagaaag 313

255 TGAATCTTTTGAAGTTTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 293

Search completed: December 9, 2001, 09:36:01

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